

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:23:23 ; Search time 106.32 Seconds
(without alignments)
399.753 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 613
Sequence: 1 MR1MLFTAILAFSLAQSGF.....DVNQENVPSFGILKYPPRAE 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3516493 seqs, 351254056 residues

Total number of hits satisfying chosen parameters: 3516493

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
- 17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
- 18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
- 19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US60_MERGED_COMB.pep1.*
- 26: /cgn2_6/ptodata/2/paa/US10_MERGED_COMB.pep1.*
- 27: /cgn2_6/ptodata/2/paa/US09_MERGED_COMB.pep2.*
- 28: /cgn2_6/ptodata/2/paa/US09_MERGED_COMB.pep1.*
- 29: /cgn2_6/ptodata/2/paa/US08_MERGED_COMB.pep1.*
- 30: /cgn2_6/ptodata/2/paa/US07_MERGED_COMB.pep1.*
- 31: /cgn2_6/ptodata/2/paa/US06_MERGED_COMB.pep1.*
- 32: /cgn2_6/ptodata/2/paa/US06_MERGED_COMB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	610	99.5	121 14	US-09-086-078-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-086-078-2
; Sequence 2, Application US/09086078
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NEUROKININ B PRECURSORS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; CITY: Seattle
; STREET: 1201 Eastlake Ave. E.
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,078
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

2	610	99.5	121	15	US-09-111-901-2	Sequence 2, Appli
3	610	99.5	121	15	US-09-152-060-68	Sequence 68, Appl
4	610	99.5	121	22	US-09-852-659-68	Sequence 68, Appl
5	610	99.5	121	22	US-09-852-797-68	Sequence 68, Appl
6	610	99.5	121	22	US-09-853-161-68	Sequence 68, Appl
7	610	99.5	121	26	US-10-058-993-68	Sequence 2248, Ap
8	610	99.5	137	1	PCT-US01-03800A-2248	Sequence 2248, Ap
9	609	99.3	121	15	US-09-152-060-85	Sequence 85, Appl
10	609	99.3	121	22	US-09-852-659-85	Sequence 85, Appl
11	609	99.3	121	22	US-09-852-797-85	Sequence 85, Appl
12	609	99.3	121	22	US-09-853-161-85	Sequence 85, Appl
13	609	99.3	121	26	US-10-058-993-85	Sequence 85, Appl
14	592.5	96.7	122	12	US-08-879-995-1	Sequence 1, Appli
15	592.5	96.7	122	18	US-09-437-860-1	Sequence 1, Appli
16	539	87.9	108	22	US-09-834-366-13657	Sequence 13657, A
17	539	87.9	108	24	US-60-197-873-13657	Sequence 13657, A
18	487	79.4	135	21	US-09-709-238-359	Sequence 359, App
19	487	79.4	135	23	US-09-929-404-357	Sequence 157, App
20	487	79.4	135	23	US-09-941-992-359	Sequence 359, App
21	487	79.4	135	26	US-10-052-586-444	Sequence 444, App
22	487	79.4	135	26	US-10-081-056-170	Sequence 170, App
23	487	79.4	135	27	US-09-989-723-359	Sequence 359, App
24	487	79.4	135	27	US-09-989-723-359	Sequence 359, App
25	487	79.4	135	27	US-09-989-723-359	Sequence 359, App
26	487	79.4	135	27	US-09-990-436-359	Sequence 359, App
27	487	79.4	135	27	US-09-990-444-359	Sequence 359, App
28	487	79.4	135	27	US-09-989-721-359	Sequence 359, App
29	487	79.4	135	27	US-09-989-722-359	Sequence 359, App
30	487	79.4	135	27	US-09-989-725-359	Sequence 359, App
31	487	79.4	135	27	US-09-989-726-359	Sequence 359, App
32	487	79.4	135	27	US-09-989-728-359	Sequence 359, App
33	487	79.4	135	27	US-09-989-731-359	Sequence 359, App
34	487	79.4	135	27	US-09-989-732-359	Sequence 359, App
35	487	79.4	135	27	US-09-989-732-359	Sequence 359, App
36	487	79.4	135	27	US-09-989-732-359	Sequence 359, App
37	487	79.4	135	27	US-09-989-734-359	Sequence 359, App
38	487	79.4	135	27	US-09-990-437-359	Sequence 359, App
39	487	79.4	135	27	US-09-990-438-359	Sequence 359, App
40	487	79.4	135	27	US-09-990-440-359	Sequence 359, App
41	487	79.4	135	27	US-09-989-279-359	Sequence 359, App
42	487	79.4	135	27	US-09-989-279-359	Sequence 359, App
43	487	79.4	135	27	US-09-990-439-359	Sequence 359, App
44	487	79.4	135	27	US-09-990-562-359	Sequence 359, App
45	487	79.4	135	27	US-09-997-529-359	Sequence 359, App

TEL/FAX:

US-09-086-078-2

Qv 1 MRTMT.1

Ov 121 F 121

RESULTS

INVENTOR: ROSEN, STEVEN
: TITLE OF INVENTION: NOVEL COMPOUNDS

; EARLIER FILING DATE: 1997-03-30

; EARLIER FILING DATE: 1997-05-30

;; EARLIER APPLICATION NUMBER: 60/048,189

; EARLIER APPLICATION NUMBER: 60/057,765

; EARLIER FILING DATE: 1997-09-05

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/068,368

; NUMBER OF SEQ ID NOS: 118

```
; SOFTWARE: PatentIn Ver. 2.0
```

```

: LENGTH: 121

```

: TYPE: PRT

PS-09-152-060-68

2
 2
 2
 2
 1
 2
 4
 2
 2
 2

Query Match 99.5%: score 6

Query Match	99.5%	Score
Best Local Similarity	99.3%	Pred

Matchless TT5; Cruiser valve U; Missile

0-7 1 MDYMT I EER T T AECY K OCEC R VCKV EDC OEEYNY

100

UP I MRIMLLF TAILAFSLAQSF GAVCKEPQE EVV

	61	LKALSQASTDPKESTSPEKRDMHDFVVGXMGKRSVPDSDPTDVNQENVPSFGILKYPPRA	120
Qy			
	61	LKALSQASTDPKESTSPEKRDMHDFVGLMGKRSVPDSDPTDVNQENVPSFGILKYPPRA	120
D _b			
	121	E	121
Qy		-	
	121	E	121
D _b			

```

RESULT      4
US-09-852-659-68
; Sequence 68, Application US/09852659
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659-68

```

[illegible]

RESULT 5
US-09-852-797-68
; Sequence 68, Application US/09852797
; GENERAL INFORMATION:

```

: APPLICANT: Rosen et al.
: TITLE OF INVENTION: 28 Human Secreted Proteins
: FILE REFERENCE: P2003P2
: CURRENT APPLICATION NUMBER: US/09/852,797
: CURRENT FILING DATE: 2001-05-11
: PRIORITY APPLICATION NUMBER: 60/265,583
: PRIORITY FILING DATE: 2001-02-02
: PRIORITY APPLICATION NUMBER: 09/152,060
: PRIORITY FILING DATE: 1998-09-11
: PRIORITY APPLICATION NUMBER: PCT/US98/04858
: PRIORITY FILING DATE: 1998-03-12
: PRIORITY APPLICATION NUMBER: 60/040,762
: PRIORITY FILING DATE: 1997-03-14
: PRIORITY APPLICATION NUMBER: 60/040,710
: PRIORITY FILING DATE: 1997-03-14
: PRIORITY APPLICATION NUMBER: 60/050,934
: PRIORITY FILING DATE: 1997-05-30
: PRIORITY APPLICATION NUMBER: 60/048,100
: PRIORITY FILING DATE: 1997-05-30
: PRIORITY APPLICATION NUMBER: 60/048,357
: PRIORITY FILING DATE: 1997-05-30
: PRIORITY APPLICATION NUMBER: 60/048,189
: PRIORITY FILING DATE: 1997-05-30
: PRIORITY APPLICATION NUMBER: 60/057,765
: PRIORITY FILING DATE: 1997-09-05
: PRIORITY APPLICATION NUMBER: 60/048,970
: PRIORITY FILING DATE: 1997-06-06
: PRIORITY APPLICATION NUMBER: 60/068,368
: PRIORITY FILING DATE: 1997-12-19
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 68
: LENGTH: 121
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-852,797-68

```

	Query Match	99.5%	Score 610;	DB 22;	Length 121;
	Best Local Similarity	98.3%;	Pred. No. 1.5e-62;		
	Matches 119; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0
Qy	1 MRIMLLFTAILAFSLAQSGFAGVCKPEQEEVPVGGGRSKRDPDLYQLLQRLFKSHSSLEGL 60 				
Dd	1 MRIMLLFTAILAFSLAQSGFAGVCKPEQEEVPVGGGRSKRDPDLYQLLQRLFKSHSSLEGL 60 				
Qy	61 LKALSOXSTDPKESTSPBKRMDHDFVGLMGKRSVQPDSPTDVNQENVPFGILKYPPRA 120 				
Dd	61 LKALSQASTDPKESTSPBKRMDHDFVGLMGKRSVQPDSPTDVNQENVPFGILKYPPRA 120 				

```

RESULT      6
US-09-853-161-68
? Sequence 68, Application US/09853161
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: 28 Human Secreted Proteins
? FILE REFERENCE: P2003p3
? CURRENT APPLICATION NUMBER: US/09/853,161
? CURRENT FILING DATE: 2001-05-11
? PRIOR APPLICATION NUMBER: 60/265,583
? PRIOR FILING DATE: 2001-02-02
? PRIOR APPLICATION NUMBER: 09/152,060
? PRIOR FILING DATE: 1998-09-11
? PRIOR APPLICATION NUMBER: PCT/US98/04858
? PRIOR FILING DATE: 1998-03-12
? PRIOR APPLICATION NUMBER: 60/040,762
? PRIOR FILING DATE: 1997-03-14
? PRIOR APPLICATION NUMBER: 60/040,710

```

; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-68

Query Match 99.5%; Score 610; DB 22; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.5e-62;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGFAGVCKEPEEVVPGGGRKRDPLDYQLLQRLFKSHSLSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGFAGVCKEPEEVVPGGGRKRDPLDYQLLQRLFKSHSLSLEGL 60

QY 61 LKALSOXSTDPKESTSPEKRDMDHDFVGLMGKRSVQPSPTDYNQENVPSFGILKYPPRA 120
Db 61 LKALSOASTDPKESTSPEKRDMDHDFVGLMGKRSVQPSPTDYNQENVPSFGILKYPPRA 120

QY 121 E 121
Db 121 E 121

RESULT 7
US-10-058-993-68
; Sequence 68, Application US/10058993
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189

; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-68

Query Match 99.5%; Score 610; DB 26; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.5e-62;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGFAGVCKEPEEVVPGGGRKRDPLDYQLLQRLFKSHSLSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGFAGVCKEPEEVVPGGGRKRDPLDYQLLQRLFKSHSLSLEGL 60

QY 61 LKALSOXSTDPKESTSPEKRDMDHDFVGLMGKRSVQPSPTDYNQENVPSFGILKYPPRA 120
Db 61 LKALSOASTDPKESTSPEKRDMDHDFVGLMGKRSVQPSPTDYNQENVPSFGILKYPPRA 120

QY 121 E 121
Db 121 E 121

RESULT 8
PCT-US01-03800A-2248
; Sequence 2248, Application PC/TUS0103800A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: PCT/US01/03800A
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2248
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03800A-2248

Query Match 99.5%; Score 610; DB 1; Length 137;
Best Local Similarity 98.3%; Pred. No. 1.8e-62;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGFAGVCKEPEEVVPGGGRKRDPLDYQLLQRLFKSHSLSLEGL 60
Db 17 MRIMLLFTAILAFSLAQSGFAGVCKEPEEVVPGGGRKRDPLDYQLLQRLFKSHSLSLEGL 76

QY 61 LKALSOXSTDPKESTSPEKRDMDHDFVGLMGKRSVQPSPTDYNQENVPSFGILKYPPRA 120
Db 77 LKALSOASTDPKESTSPEKRDMDHDFVGLMGKRSVQPSPTDYNQENVPSFGILKYPPRA 136

QY 121 E 121
Db 137 E 137


```

RESULT 9
US-09-152-060-85
; Sequence 85, Application US/09152060
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003Pl.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-85

Query Match          99,3%; Score 609; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MRIMLLFTAILAFSLAQSFGAVCKPEQEVVPGGSRKRDPLQLQLRKFKSHSLEGL 60
   |||||
Db 1 MRIMLLFTAILAFSLAQSFGAVCKPEQEVVPGGSRKRDPLQLQLRKFKSHSLEGL 60
   |||||
QY 61 LKALSOXSTDPKSTSPKRDHDMHFFVGMGKRVSQVDPDPTDVNOENVPSEGIKYPPRA 120
   |||||
Db 61 LKALSOXSTDPKSTSPKRDHDMHFFVGMGKRVSQVDPDPTDVNOENVPSEGIKYPPRA 120
   |||||
QY 121 E 121
Db 121 E 121

RESULT 10
US-09-852-659-85
; Sequence 85, Application US/09852659
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583

```

```

; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-797-85

```

```

Query Match          99.3%; Score 609; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
   |||||||
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60

QY 61 LKALSOXSTDPKESTPEKRDMDHDFVGMGKRSVQDPDPTDYNQENVPFSGILKYPPRA 120
   |||||||
Db 61 LKALSOXSTDPKESTPEKRDMDHDFVGMGKRSVQDPDPTDYNQENVPFSGILKYPPRA 120

QY 121 E 121
Db 121 E 121

```

```

RESULT 12
US-09-853-161-85
; Sequence 85, Application US/09853161
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357

```

```

; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-853-161-85

```

```

Query Match          99.3%; Score 609; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
   |||||||
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60

QY 61 LKALSOXSTDPKESTPEKRDMDHDFVGMGKRSVQDPDPTDYNQENVPFSGILKYPPRA 120
   |||||||
Db 61 LKALSOXSTDPKESTPEKRDMDHDFVGMGKRSVQDPDPTDYNQENVPFSGILKYPPRA 120

QY 121 E 121
Db 121 E 121

```

```

RESULT 13
US-10-058-993-85
; Sequence 85, Application US/10058993
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30

```

;; PRIOR APPLICATION NUMBER: 60/048,189
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,357
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/040,710
;; PRIOR FILING DATE: 1997-03-14
;; PRIOR APPLICATION NUMBER: 60/040,762
;; PRIOR FILING DATE: 1997-03-14
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 85
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (67)
;; OTHER INFORMATION: Xaa equals any amino acid
;; NAME/KEY: SITE
;; LOCATION: (89)
;; OTHER INFORMATION: Xaa equals any amino acid
US-10-050-993-85

Query Match 99.3%; Score 609; DB 26; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60

Qy 61 LKALSOXSTDPKESTSPKRDHDFVGMGKRVSQVQPSPTDVNOENVPSFGILKYPPRA 120
Db 61 LKALSOXSTDPKESTSPKRDHDFVGMGKRVSQVQPSPTDVNOENVPSFGILKYPPRA 120

Qy 121 E 121
Db 121 E 121

RESULT 14
US-08-879-995-1
;; Sequence 1, Application US/08879995
;; GENERAL INFORMATION:
;; APPLICANT: Hillman, Jennifer L.
;; APPLICANT: Lal, Preeti
;; APPLICANT: Kaser, Matthew R.
;; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/879,995
;; FILING DATE: Herewith
;; CLASSIFICATION: ?
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0326 US

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: BRAITUT03
;; CLONE: 2109906
US-08-879-995-1

Query Match 96.7%; Score 592.5; DB 12; Length 122;
Best Local Similarity 95.9%; Pred. No. 1.7e-60;
Matches 117; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60

Qy 61 LKALSOXSTDPKESTSPKRDHDFVGMGKRVSQVQPSPTDVNOENVPSFGILKYPPR 119
Db 61 LKALSOXSTDPKESTSPKRDHDFVGMGKRVSQVQPSPTDVNOENVPSFGILKYPPR 120

Qy 120 AE 121
Db 121 AE 122

RESULT 15
US-09-437-860-1
;; Sequence 1, Application US/09437860
;; GENERAL INFORMATION:
;; APPLICANT: Hillman, Jennifer L.
;; APPLICANT: Lal, Preeti
;; APPLICANT: Kaser, Matthew R.
;; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/437,860
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/879,995
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0326 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
US-09-437-860-1

Query Match 96.7%; Score 592.5; DB 18; Length 122;
Best Local Similarity 95.9%; Pred. No. 1.7e-60;
Matches 117; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 1 MRIMLLFTAILAFSLAQSEFGAVCKEQEVPVGGGRSKRDPDLYQLQLRKFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSEFGAVCKEQEVPVGGGRSKRDPDLYQLQLRKFKSHSLEGL 60
QY 61 LKALSQXSTDPKESTSPKRDMDHDFVGMGKRVSQVOPDPTDV - NOENVPSFGILKYPPR 119
Db 61 LKALSQASTDPKESTSPKRDMDHDFVGLMGKRVSQVOPDPTDV - NOENVPSFGILKYPPR 120
QY 120 AE 121
Db 121 AE 122

Search completed: May 3, 2002, 12:26:39
Job time: 196 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 16:38:37 ; Search time 8.32 Seconds
(without alignments)
171.347 Million cell updates/sec

Title: US-09-852-659-85

Perfect score: 613

Sequence: 1 MRIMLLFTAILAFSLAQSGF.....DVNOENVPSGILKYPRAE 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 59194 seqs, 11781848 residues

Total number of hits satisfying chosen parameters: 59194

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	487	79.4	135	5	US-09-991-150-359
2	487	79.4	135	6	US-10-119-480-108
3	68	11.1	452	5	US-09-563-794B-140
4	65.5	10.7	911	1	PCT-US02-06415-6
5	65.5	10.7	911	1	PCT-US02-06415-6
6	64.5	10.5	1005	1	PCT-US02-10133-2
7	64.5	10.5	1005	5	US-09-486-861A-2
8	63	10.3	197	6	US-10-121-746-16
9	63	10.3	206	1	PCT-US02-09921-864
10	63	10.3	812	5	US-09-573-655B-347
11	63	10.3	812	5	US-09-573-655B-665
12	62	10.1	353	5	US-09-647-701A-2
13	62	10.1	452	5	US-09-563-794B-2
14	62	10.1	1394	4	US-08-945-917B-57
15	62	10.1	1449	4	US-08-945-917B-58
16	62	10.1	1528	4	US-08-945-917B-3
17	62	10.1	1583	4	US-08-945-917B-4
18	61.5	10.0	843	5	US-09-573-655B-413
19	61.5	10.0	1005	1	PCT-US02-10824-111
20	61.5	10.0	2063	1	PCT-US02-08253-204
21	61	10.0	518	5	US-09-573-655B-1620
22	61	10.0	518	5	US-09-573-655B-2273
23	60.5	9.9	828	5	US-09-540-209B-7655
24	60.5	9.9	3210	1	PCT-US02-10824-148
25	60	9.8	176	5	US-09-540-209B-8505
26	60	9.8	999	7	US-60-365-264-226

27	59.5	9.7	723	5	US-09-540-209B-5947	Sequence 5947, Ap
28	58.5	9.5	299	5	US-09-540-209B-9990	Sequence 9990, Ap
29	58.5	9.5	366	5	US-09-540-209B-6699	Sequence 6699, Ap
30	58.5	9.5	422	5	US-09-573-655B-800	Sequence 800, App
31	58.5	9.5	422	5	US-09-573-655B-1162	Sequence 1162, Ap
32	58.5	9.5	1596	5	US-09-902-432-4	Sequence 4, Appli
33	58.5	9.5	2067	1	PCT-US02-09944-778	Sequence 778, App
34	58	9.5	561	5	US-09-573-655B-2000	Sequence 2000, Ap
35	58	9.5	655	1	PCT-US02-09808-29	Sequence 29, Appl
36	57.5	9.4	86	1	PCT-US02-09921-873	Sequence 873, App
37	57.5	9.4	183	5	US-09-573-655B-1836	Sequence 1836, Ap
38	57.5	9.4	472	1	PCT-US02-09473-2	Sequence 2, Appli
39	57	9.3	124	1	PCT-US02-09820-10	Sequence 10, Appl
40	57	9.3	826	1	PCT-US02-08866-10	Sequence 10, Appl
41	57	9.3	826	1	PCT-US02-08864-6	Sequence 6, Appli
42	57	9.3	826	1	PCT-US02-08946-2	Sequence 2, Appli
43	57	9.3	826	1	PCT-US02-08946-5	Sequence 5, Appli
44	57	9.3	826	1	PCT-US02-08946-6	Sequence 6, Appli
45	57	9.3	826	1	PCT-US02-08946-7	Sequence 7, Appli

ALIGNMENTS

RESULT

US-09-991-150-359
; Sequence 359, Application US/09991150
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC48
CURRENT APPLICATION NUMBER: US/09/991,150
CURRENT FILING DATE: 2001-11-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 532
SEQ ID NO 359
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-09-991-150-359

Query Match 79.4%; Score 487; DB 5; Length 135;
Best Local Similarity 95.0%; Pred. NO. 1.3e-48;
Matches 96; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGFVPGGSRKRDPLDYLQRLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGFVPGGSRKRDPLDYLQRLFKSHSLEGL 60

```

Qy 61 LKALSQXSTDPKESTSPKSRDMHDFEVGXMGRSVQPDSP 101
      | | | | | | | | | | | | | | | | | | | | | | |
Db 61 LKALSQASTDPKESTSPKSRDMHDFEVGLMGKRSVPQSGT 101

```

```

RESULT      2
US-10-119-480-108
; Sequence 108, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Collin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 108
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-108

```

```

Qy      61 LKALSQXSTDPKESTSPKSRMDHDFVVGXMGKRSVQPSPT 101
        | | | | | | | | | | | | | | | | | | | | | | |
Db      61 LKALSQASTDPKESTSPKSRMDHDFVVGXMGKRSVQPEGT 101

```

```

RESULT      3
US-09-563-794B-140
; Sequence 140, Application US/09563794B
; GENERAL INFORMATION:
; APPLICANT: KRUGER, MARTIN
; APPLICANT: WELCH, PETER J.
; APPLICANT: BARBER, JACK R.
; TITLE OF INVENTION: CELLULAR REGULATORS OF INFECTIOUS AGENTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 039316-0801
; CURRENT APPLICATION NUMBER: US/09/563.794B
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-563-794B-140

Query Match      11.1%; Score 68; DB 5; Length 452;
Best Local Similarity 27.7%; Pred. No. 2.6;
Matches 23; Conservative 19; Mismatches 37; Indels 4; Gaps 3

QY      40  DPDLVQLLQRLKPKSHSLLEGLLKALQSXSTDPKSTSPKRL--DMHDFV-VGXMGKRSVQ 96

```

```

Db      111  DVALHEYVD-LFRAYDASLAMLRKGGQESTPEVPGKGKKTKTVEGRDFIGVDSTGKRLLF 169
QY      97  PDSEPTDVNQENVPSFGILKYPPR 119
Db     170  MANEADDEELVIGKSILOKHPR 192

```

```

RESULT      4
PCT-US02-06415-6
; Sequence 6, Application PC/TUS0206415
; GENERAL INFORMATION:
; APPLICANT: St. Elizabeth's Medical Center, Inc.
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019wo
; CURRENT APPLICATION NUMBER: PCT/US02/06415
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-06415-6

```

Query Match	10.7%	Score 65.5;	DB 1;	Length 911;
Best Local Similarity	23.9%;	Pred. No. 14;		
Matches	32;	Conservative 16;	Mismatches 59;	Indels 27; Gaps
Qy	5	LFTAILAFSLAQSFQAVCKEPOEEVVPGGGRSK-----RDPDLVQLLQRLFKSH	54	
	: :	: :	: :	
Db	102	LTFWSLLELRVFYTKGVLLDQETSLAGVANOLLRFIEDQIRPDREELRALLLKH	161	
	: :	: :	: :	
Qy	55	S-----SLEGGLKASQXSTDPKESTSPEKRMDHOFVFGVMGKRSPQDPSDVNQENV	108	
	: :	: :	: :	
Db	162	SHAGEALGAVRPVLTRSGDRSQPLLPHSSLSLETQLFCEQGDTGEHSPTS-----	214	
	: :	: :	: :	
Qy	109	PSFGIL-KYPFRAE	121	
Db	215	--GILEKIPDPSE	225	

```

RESULT      5
PCT-US02-06415-8
; Sequence 8, Application PC/TUS0206415
; GENERAL INFORMATION:
; APPLICANT: St. Elizabeth's Medical Center, Inc.
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019WO
; CURRENT APPLICATION NUMBER: PCT/US02/06415
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-06415-8

```

```

Query Match      10.7%; Score 65.5; DB 1; Length 911;
Best Local Similarity 23.9%; Pred. No. 14;
Matches 32; Conservative 16; Mismatches 59; Indels 27; Gaps

QY 5 LLFTAILAFSLAOSFGAVCKEPOEEVPPGGRSK-----RDPDLQVLLQRLFKSH 54
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 102 LTFWSLLELRVFTKGVLLDLDTSLAGVANOLLDFIEFDIOIRPORELLRALLKKH 161
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

QY 6 LFTAILAFSLAQSFQAVCKEPEQEEVPPGGGRSKRDPDLYOLLORLFKSHSSLEGLLKALS 65

RESULT 9
PCT-US02-09921-864
; Sequence 864, Application PC/TUS0209921
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFOE, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Barryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E. L.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHER, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.

[illegible]

; APPLICANT: KRUGER, MARTIN
; APPLICANT: WELCH, PETER J.
; APPLICANT: BARBER, JACK R.
; TITLE OF INVENTION: CELLULAR REGULATORS OF INFECTIOUS AGENTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 039316-0801
; CURRENT APPLICATION NUMBER: US/09/563,794B
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-794B-2

Query Match 10.1%; Score 62; DB 5; Length 452;
Best Local Similarity 26.5%; Pred. No. 14;
Matches 22; Conservative 19; Mismatches 38; Indels 4; Gaps 3;
Qy 40 DPDLVQLQLRFLKSHSLGGLKALSOXSTDPKSTSPKRDHDFV-GVXMGKRSVQ 96
Db 111 DVALHEVD-LFRAYDASLMLKRGQDSIEVPQCKGKRAVEQDFIGVDSTGKRLIF 169
Qy 97 PDSPTDVNQENVPSFGILKYPPR 119
Db 170 MANEADLDEELVINGSLIQKHPR 192

RESULT 14
US-08-945-917B-57
; Sequence 57, Application US/08945917B
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/08/945,917B
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 1394
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-08-945-917B-57

Query Match 10.1%; Score 62; DB 4; Length 1394;
Best Local Similarity 25.4%; Pred. No. 63;
Matches 31; Conservative 11; Mismatches 50; Indels 30; Gaps 5;
Qy 15 LAQSFQAVCKEPQEEVPGGGRKRDPLYQLLQRLFKSHSLGGLKALSOXSTDPKES 74
Db 250 ISQODSKRCRKSSEEEGCGYAGFNSTP-----TSSSTEG---SLSMHSTSSKSS 295
Qy 75 TSPEKRMHD-----FFVGMGKRSVQPSDPTDVNQ--ENVPSFGI-----LKYPP 118
Db 296 TSDEKSPSSDDLTLNASIVTAIROPIATPVSPNIINKPVEKPTLAVKGVKSTAKKDDP 355
Qy 119 RA 120
Db 356 PA 357

RESULT 15
US-08-945-917B-58
; Sequence 58, Application US/08945917B
; GENERAL INFORMATION:

; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/08/945,917B
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 1449
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-08-945-917B-58

Query Match 10.1%; Score 62; DB 4; Length 1449;
Best Local Similarity 25.4%; Pred. No. 66;
Matches 31; Conservative 11; Mismatches 50; Indels 30; Gaps 5;
Qy 15 LAQSFQAVCKEPQEEVPGGGRKRDPLYQLLQRLFKSHSLGGLKALSOXSTDPKES 74
Db 250 ISQODSKRCRKSSEEEGCGYAGFNSTP-----TSSSTEG---SLSMHSTSSKSS 295
Qy 75 TSPEKRMHD-----FFVGMGKRSVQPSDPTDVNQ--ENVPSFGI-----LKYPP 118
Db 296 TSDEKSPSSDDLTLNASIVTAIROPIATPVSPNIINKPVEKPTLAVKGVKSTAKKDDP 355
Qy 119 RA 120
Db 356 PA 357

Search completed: May 3, 2002, 16:39:49
Job time: 72 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:27:23 ; Search time 106.55 Seconds
(without alignments)
398.890 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRIMLLFTAILAFSLAQSG.....DVNQENVPFGILKYPPRAE 121

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 3516493 seqs, 351254056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3516493

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending Patents AA.Main.*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
- 17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
- 18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
- 19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US101_MERGED_COMB.pep1.*
- 26: /cgn2_6/ptodata/2/paa/US102_MERGED_COMB.pep1.*
- 27: /cgn2_6/ptodata/2/paa/US103_MERGED_COMB.pep2.*
- 28: /cgn2_6/ptodata/2/paa/US104_MERGED_COMB.pep1.*
- 29: /cgn2_6/ptodata/2/paa/US105_MERGED_COMB.pep1.*
- 30: /cgn2_6/ptodata/2/paa/US106_MERGED_COMB.pep1.*
- 31: /cgn2_6/ptodata/2/paa/US107_MERGED_COMB.pep1.*
- 32: /cgn2_6/ptodata/2/paa/US108_MERGED_COMB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	98.3	121	15	US-09-152-060-85
					Sequence 85, Appl

75	54.5	135	27	US-09-997-666-359	Sequence 359, App	148	7	5.8	300	21	US-09-771-161-116	Sequence 116, App
76	54.5	135	27	US-09-997-683-359	Sequence 359, App	149	7	5.8	300	21	US-09-771-161A-116	Sequence 116, App
77	54.5	135	27	US-09-998-041-359	Sequence 359, App	150	7	5.8	316	24	US-60-213-847-1199	Sequence 1199, App
78	54.5	135	27	US-09-998-156-359	Sequence 359, App	151	7	5.8	338	27	US-09-708-427-74452	Sequence 74452, A
79	54.5	135	27	US-09-998-156-359	Sequence 359, App	152	7	5.8	338	27	US-09-818-990-4	Sequence 4, Appl
80	54.5	135	27	US-09-998-156-359	Sequence 359, App	153	7	5.8	376	22	US-09-708-427-74451	Sequence 74451, A
81	54.5	135	27	US-09-998-243-359	Sequence 359, App	154	7	5.8	381	22	US-09-708-427-74450	Sequence 74450, A
82	54.5	135	27	US-09-997-333-359	Sequence 359, App	155	7	5.8	393	27	US-09-818-990-8	Sequence 8, Appl
83	54.5	135	27	US-09-997-333-359	Sequence 359, App	156	7	5.8	401	22	US-09-614-150-28950	Sequence 28950, A
84	54.5	135	27	US-09-997-529-359	Sequence 359, App	157	7	5.8	405	27	US-09-391-631-283	Sequence 283, App
85	54.5	135	27	US-09-997-641-359	Sequence 359, App	158	7	5.8	415	17	US-09-818-990-6	Sequence 6, Appl
86	54.5	135	27	US-09-997-857-359	Sequence 359, App	159	7	5.8	419	22	US-09-770-509-10	Sequence 10, Appl
87	54.5	135	27	US-09-990-711-359	Sequence 359, App	160	7	5.8	420	21	US-09-818-990-10	Sequence 10, Appl
88	54.5	135	27	US-09-989-293A-359	Sequence 359, App	161	7	5.8	459	22	US-09-543-681A-6768	Sequence 6768, App
89	54.5	135	27	US-09-989-293A-359	Sequence 359, App	162	7	5.8	465	19	US-09-807-239-42	Sequence 42, Appl
90	54.5	135	28	US-09-989-729A-359	Sequence 359, App	163	7	5.8	483	22	US-09-583-110-4060	Sequence 4060, App
91	54.5	137	1	PCT-US01-03800A-2248	Sequence 2248, App	164	7	5.8	493	19	US-09-252-991A-20533	Sequence 20533, A
92	22.3	39	15	US-09-111-901-3	Sequence 3, Appl	165	7	5.8	526	16	US-09-391-631-282	Sequence 282, App
93	22.3	39	15	US-09-111-901-3	Sequence 3, Appl	166	7	5.8	526	16	US-09-270-767-46261	Sequence 46261, A
94	23	19.0	36	US-09-152-060-108	Sequence 108, App	167	7	5.8	570	22	US-09-818-990-12	Sequence 12, Appl
95	23	19.0	36	US-09-852-659-108	Sequence 108, App	168	7	5.8	573	24	US-60-245-225-247	Sequence 247, App
96	23	19.0	36	US-09-852-797-108	Sequence 108, App	169	7	5.8	589	24	US-60-248-505-862	Sequence 862, App
97	23	19.0	36	US-09-853-161-108	Sequence 108, App	170	7	5.8	590	5	US-08-123-932A-12	Sequence 12, Appl
98	10	8.3	15	US-10-058-993-108	Sequence 108, App	171	7	5.8	590	21	US-09-771-161A-206	Sequence 206, App
99	10	8.3	15	US-09-152-060-109	Sequence 109, App	172	7	5.8	590	21	US-09-771-161A-207	Sequence 207, App
100	10	8.3	15	US-09-852-659-109	Sequence 109, App	173	7	5.8	590	21	US-09-771-161A-208	Sequence 208, App
101	10	8.3	15	US-09-852-797-109	Sequence 109, App	174	7	5.8	590	23	US-09-972-694-2	Sequence 2, Appl
102	10	8.3	15	US-09-853-161-109	Sequence 109, App	175	7	5.8	608	27	US-09-851-686-5	Sequence 5, Appl
103	10	8.3	92	US-10-058-993-109	Sequence 30, Appl	176	7	5.8	608	27	US-60-191-637-18659	Sequence 18659, A
104	10	8.3	116	US-08-879-995-4	Sequence 4, Appl	177	7	5.8	608	27	US-09-614-150-18603	Sequence 18603, A
105	10	8.3	126	US-09-437-860-4	Sequence 4, Appl	178	7	5.8	640	1	PCT-US01-08631-46868	Sequence 46868, A
106	10	8.3	126	US-08-879-995-3	Sequence 3, Appl	179	7	5.8	702	19	US-09-506-720-208	Sequence 208, App
107	10	8.3	126	US-09-437-860-3	Sequence 3, Appl	180	7	5.8	702	28	US-09-506-720B-208	Sequence 208, App
108	8	6.6	10	US-08-153-847-4	Sequence 4, Appl	181	7	5.8	741	25	US-60-361-742-1678	Sequence 1678, App
109	8	6.6	10	US-08-166-437-3	Sequence 3, Appl	182	7	5.8	754	22	US-09-818-990-14	Sequence 14, Appl
110	8	6.6	10	US-08-171-134-4	Sequence 4, Appl	183	7	5.8	913	18	US-09-488-725A-6009	Sequence 6009, App
111	8	6.6	10	US-08-235-401-4	Sequence 4, Appl	184	7	5.8	1145	21	US-09-758-759-167	Sequence 167, App
112	8	6.6	10	US-08-259-266-4	Sequence 4, Appl	185	7	5.8	1245	27	US-09-716-964A-87	Sequence 87, Appl
113	8	6.6	10	US-08-271-708-4	Sequence 4, Appl	186	7	5.8	1251	27	US-09-708-427-18424	Sequence 18424, A
114	8	6.6	10	US-08-279-330-4	Sequence 4, Appl	187	7	5.8	1320	22	US-09-818-990-2	Sequence 2, Appl
115	8	6.6	10	US-08-343-750-4	Sequence 4, Appl	188	7	5.8	1316	27	US-09-708-427-18423	Sequence 18423, A
116	8	6.6	10	US-08-387-056-4	Sequence 4, Appl	189	6	5.0	9	20	US-09-657-276-545	Sequence 545, App
117	8	6.6	10	US-08-408-238-4	Sequence 4, Appl	190	6	5.0	10	3	US-07-737-371A-43	Sequence 43, Appl
118	8	6.6	10	US-09-111-901-4	Sequence 4, Appl	191	6	5.0	10	3	US-07-737-371A-44	Sequence 44, Appl
119	8	6.6	10	US-09-152-060-110	Sequence 110, App	192	6	5.0	10	3	US-07-737-371D-43	Sequence 43, Appl
120	8	6.6	10	US-09-582-137A-3	Sequence 3, Appl	193	6	5.0	10	3	US-07-737-371D-44	Sequence 44, Appl
121	8	6.6	10	US-09-657-276-544	Sequence 544, App	194	6	5.0	10	20	US-09-657-276-546	Sequence 546, App
122	8	6.6	10	US-09-657-276-573	Sequence 573, App	195	6	5.0	10	24	US-60-272-565-51	Sequence 51, Appl
123	8	6.6	10	US-09-852-659-110	Sequence 110, App	196	6	5.0	20	17	US-09-828-708-25	Sequence 25, Appl
124	8	6.6	10	US-09-852-797-110	Sequence 110, App	197	6	5.0	20	1	PCT-US00-12788-455	Sequence 455, App
125	8	6.6	10	US-09-853-161-110	Sequence 110, App	198	6	5.0	20	27	US-09-985-480-455	Sequence 455, App
126	8	6.6	10	US-10-058-993-110	Sequence 110, App	199	6	5.0	26	11	US-08-787-738B-18	Sequence 18, Appl
127	8	6.6	11	US-09-657-276-547	Sequence 547, App	200	6	5.0	26	11	US-08-787-738B-18	Sequence 18, Appl
128	7	5.8	30	US-60-196-174-837	Sequence 837, App	201	6	5.0	26	12	US-08-873-601-14	Sequence 14, Appl
129	7	5.8	54	US-60-160-209-3775	Sequence 3775, App	202	6	5.0	26	13	US-08-963-368-18	Sequence 18, Appl
130	7	5.8	106	US-60-187-385-754	Sequence 754, App	203	6	5.0	26	15	US-09-157-748-21	Sequence 21, Appl
131	7	5.8	147	US-09-543-681A-5629	Sequence 5629, App	204	6	5.0	26	16	US-09-208-827-19	Sequence 19, Appl
132	7	5.8	160	US-09-771-161-115	Sequence 115, App	205	6	5.0	26	16	US-09-285-912-81	Sequence 81, Appl
133	7	5.8	160	US-09-771-161A-115	Sequence 115, App	206	6	5.0	26	16	US-09-285-912A-81	Sequence 81, Appl
134	7	5.8	181	US-09-708-427-65725	Sequence 65725, A	207	6	5.0	26	16	US-09-293-670-24	Sequence 24, Appl
135	7	5.8	206	US-09-595-330A-1345	Sequence 1345, App	208	6	5.0	26	18	US-09-419-381-65	Sequence 65, Appl
136	7	5.8	209	US-09-620-394B-7457	Sequence 7457, App	209	6	5.0	26	19	US-09-578-030-22	Sequence 22, Appl
137	7	5.8	220	US-09-134-000-3991	Sequence 3991, App	210	6	5.0	26	21	US-09-792-629-73	Sequence 73, Appl
138	7	5.8	230	US-60-324-109-27604	Sequence 27604, A	211	6	5.0	26	21	US-09-792-630-67	Sequence 67, Appl
139	7	5.8	257	US-60-184-775-1358	Sequence 1358, App	212	6	5.0	26	22	US-09-800-170-71	Sequence 71, Appl
140	7	5.8	283	US-60-167-324-1348	Sequence 1348, App	213	6	5.0	26	26	US-10-052-940-21	Sequence 21, Appl
141	7	5.8	283	US-60-173-386-1312	Sequence 1312, App	214	6	5.0	26	26	US-10-061-395-15	Sequence 15, Appl
142	7	5.8	283	US-60-175-871-1489	Sequence 1489, App	215	6	5.0	26	26	US-10-080-376-67	Sequence 67, Appl
143	7	5.8	284	US-60-323-349-243	Sequence 243, App	216	6	5.0	26	26	US-10-096-550-18	Sequence 18, Appl
144	7	5.8	285	US-09-620-394B-7456	Sequence 7456, App	217	6	5.0	26	27	US-09-916-940-18	Sequence 18, Appl
145	7	5.8	286	US-60-191-637-41619	Sequence 41619, A	218	6	5.0	26	28	US-09-415-765A-31	Sequence 31, Appl
146	7	5.8	286	US-60-191-700-1455	Sequence 1455, App	219	6	5.0	26	28	US-09-620-580B-31	Sequence 31, Appl
147	7	5.8	286	US-09-614-150-41985	Sequence 41985, A	220	6	5.0	26	28	US-09-626-581C-31	Sequence 31, Appl

221	6	5.0	26	28	US-09-922-503-11	Sequence 11, Appl	294	6	5.0	80	21	US-09-758-446-1376	Sequence 1376, Ap
222	6	5.0	26	32	PCT-US02-02814-15	Sequence 15, Appl	295	6	5.0	81	20	US-09-617-682A-4030	Sequence 4030, Ap
223	6	5.0	28	24	US-60-182-569-1161	Sequence 1161, Ap	296	6	5.0	82	22	US-09-854-847-200	Sequence 20, Appl
224	6	5.0	36	1	PCT-US01-00663-30976	Sequence 30976, A	297	6	5.0	82	27	US-09-708-427-80033	Sequence 80033, A
225	6	5.0	36	22	US-09-864-761-3783	Sequence 3783, A	298	6	5.0	83	25	US-60-333-726-681	Sequence 681, App
226	6	5.0	36	24	US-60-236-359-20238	Sequence 20238, A	299	6	5.0	83	26	US-10-083-357-681	Sequence 681, App
227	6	5.0	36	5	US-08-188-334-25	Sequence 25, Appl	300	6	5.0	84	16	US-09-270-767-34492	Sequence 34492, A
228	6	5.0	39	27	US-09-708-427-72688	Sequence 72688, A	301	6	5.0	84	16	US-09-270-767-49709	Sequence 49709, A
229	6	5.0	40	19	US-09-538-038-796	Sequence 796, App	302	6	5.0	84	16	US-09-270-849B-180965	Sequence 180965,
230	6	5.0	41	24	US-60-170-346-2002	Sequence 2002, Ap	303	6	5.0	85	1	PCT-US00-05988-1083	Sequence 1083, Ap
231	6	5.0	41	28	US-09-455-978B-23	Sequence 23, Appl	304	6	5.0	85	1	PCT-US01-08631-34565	Sequence 34565, A
232	6	5.0	45	1	PCT-US01-29838-348	Sequence 348, App	305	6	5.0	85	12	US-08-827-356-2847	Sequence 2847, Ap
233	6	5.0	48	17	US-09-374-494-22	Sequence 42, Appl	306	6	5.0	85	19	US-09-543-681A-7741	Sequence 7741, Ap
234	6	5.0	48	22	US-09-851-138-22	Sequence 22, Appl	307	6	5.0	85	21	US-09-758-471-4958	Sequence 4958, Ap
235	6	5.0	48	24	US-60-182-093-1898	Sequence 1898, Ap	308	6	5.0	85	23	US-09-925-300-1083	Sequence 1083, Ap
236	6	5.0	50	1	PCT-US01-02723-305	Sequence 305, App	309	6	5.0	86	24	US-60-182-568-901	Sequence 901, App
237	6	5.0	50	15	US-09-146-313-49	Sequence 49, Appl	310	6	5.0	88	1	PCT-US01-01341-1286	Sequence 1286, Ap
238	6	5.0	50	21	US-09-707-351-305	Sequence 305, App	311	6	5.0	88	14	US-09-057-719-779	Sequence 779, App
239	6	5.0	50	24	US-60-182-075-59	Sequence 59, Appl	312	6	5.0	88	18	US-09-471-276-1566	Sequence 1566, Ap
240	6	5.0	55	20	US-09-617-682A-15153	Sequence 15153, A	313	6	5.0	88	21	US-09-764-864-1286	Sequence 1286, Ap
241	6	5.0	56	20	US-09-617-681A-2968	Sequence 2968, Ap	314	6	5.0	88	26	US-10-080-129-1286	Sequence 1286, Ap
242	6	5.0	56	24	US-60-170-430-1955	Sequence 1955, Ap	315	6	5.0	91	21	US-09-733-089-19111	Sequence 19111, A
243	6	5.0	56	27	US-09-675-784A-8286	Sequence 8286, Ap	316	6	5.0	91	21	US-09-816-660-19111	Sequence 19111, A
244	6	5.0	58	24	US-60-182-568-616	Sequence 616, App	317	6	5.0	91	22	US-60-171-481-1428	Sequence 1428, Ap
245	6	5.0	59	1	PCT-US01-08631-54499	Sequence 54499, A	318	6	5.0	92	13	US-08-904-468-329	Sequence 329, App
246	6	5.0	59	1	PCT-US01-08631-54502	Sequence 54502, A	319	6	5.0	92	24	US-60-192-587-1640	Sequence 1640, Ap
247	6	5.0	61	1	PCT-US01-08655-498	Sequence 498, App	320	6	5.0	92	24	US-60-192-737-1300	Sequence 1300, Ap
248	6	5.0	62	24	US-60-162-357-1430	Sequence 1430, Ap	321	6	5.0	92	24	US-60-194-091-1579	Sequence 1579, Ap
249	6	5.0	62	24	US-60-178-305-1132	Sequence 1132, Ap	322	6	5.0	92	24	US-60-194-106-796	Sequence 796, App
250	6	5.0	63	1	PCT-US01-29871-163	Sequence 163, App	323	6	5.0	93	1	PCT-US00-09071-123	Sequence 123, App
251	6	5.0	63	14	US-09-049-719-2	Sequence 2, Appl	324	6	5.0	93	16	US-09-296-622-609	Sequence 609, App
252	6	5.0	63	16	US-09-280-190-4	Sequence 4, Appl	325	6	5.0	93	24	US-60-195-134-1213	Sequence 1213, Ap
253	6	5.0	63	18	US-09-410-375-4	Sequence 4, Appl	326	6	5.0	93	28	US-09-870-759-70	Sequence 70, Appl
254	6	5.0	63	22	US-09-834-366-19528	Sequence 19528, A	327	6	5.0	94	24	US-60-170-346-1327	Sequence 1327, Ap
255	6	5.0	63	24	US-60-162-245-3023	Sequence 3023, Ap	328	6	5.0	94	24	US-60-181-996-1304	Sequence 1304, Ap
256	6	5.0	63	24	US-60-197-873-19528	Sequence 19528, A	329	6	5.0	94	24	US-60-182-093-1957	Sequence 1957, Ap
257	6	5.0	64	1	PCT-US00-14933-135	Sequence 135, App	330	6	5.0	95	24	US-60-162-247-3594	Sequence 3594, Ap
258	6	5.0	64	1	PCT-US01-00911-162	Sequence 162, App	331	6	5.0	95	24	US-60-169-840-7420	Sequence 7420, Ap
259	6	5.0	64	1	PCT-US99-15849-162	Sequence 162, App	332	6	5.0	95	24	US-60-192-587-1028	Sequence 1028, Ap
260	6	5.0	64	18	US-09-482-273-162	Sequence 162, App	333	6	5.0	96	1	PCT-US01-08656-7336	Sequence 7336, Ap
261	6	5.0	64	27	US-09-984-271-162	Sequence 162, App	334	6	5.0	96	17	US-09-325-932-166	Sequence 166, App
262	6	5.0	64	27	US-09-984-271-162	Sequence 162, App	335	6	5.0	96	17	US-09-325-932-166	Sequence 166, App
263	6	5.0	64	27	US-09-984-271-162	Sequence 162, App	336	6	5.0	96	17	US-09-327-373-166	Sequence 166, App
264	6	5.0	65	20	US-09-617-682A-4032	Sequence 4032, Ap	337	6	5.0	96	21	US-09-758-471-4924	Sequence 445, App
265	6	5.0	65	21	US-09-758-462-1490	Sequence 1490, Ap	338	6	5.0	96	21	US-09-758-471-4924	Sequence 4924, Ap
266	6	5.0	67	16	US-09-201-945-164	Sequence 164, App	339	6	5.0	97	1	PCT-US01-01354-17778	Sequence 17778, A
267	6	5.0	67	16	US-09-248-796-25479	Sequence 25479, A	340	6	5.0	97	21	US-09-764-905-17778	Sequence 17778, A
268	6	5.0	68	1	PCT-US01-01339-3050	Sequence 3050, Ap	341	6	5.0	97	21	US-09-834-366-21129	Sequence 21129, A
269	6	5.0	68	21	US-09-764-891-3050	Sequence 3050, Ap	342	6	5.0	97	22	US-09-834-366-21129	Sequence 21129, A
270	6	5.0	68	22	US-09-854-847-4	Sequence 4, Appl	343	6	5.0	97	22	US-09-147-499-7196	Sequence 7196, Ap
271	6	5.0	69	24	US-60-162-247-5063	Sequence 5063, Ap	344	6	5.0	97	24	US-60-137-873-21129	Sequence 21129, A
272	6	5.0	70	1	PCT-US00-07677-116	Sequence 116, App	345	6	5.0	97	24	US-10-092-399-17778	Sequence 17778, A
273	6	5.0	71	16	US-09-248-796-25318	Sequence 25318, A	346	6	5.0	97	26	US-09-708-427-73893	Sequence 73893, A
274	6	5.0	72	24	US-60-170-429-869	Sequence 869, App	347	6	5.0	97	26	US-09-621-976-7196	Sequence 7196, Ap
275	6	5.0	72	24	US-60-181-269-633	Sequence 633, App	348	6	5.0	98	1	PCT-US01-08656-9054	Sequence 9054, App
276	6	5.0	72	24	US-09-675-784A-12060	Sequence 12060, A	349	6	5.0	98	1	PCT-US97-02318-566	Sequence 566, App
277	6	5.0	74	22	US-09-834-366-23197	Sequence 23197, A	350	6	5.0	98	13	US-08-903-470-566	Sequence 566, App
278	6	5.0	74	24	US-60-147-499-6396	Sequence 6396, Ap	351	6	5.0	98	24	US-60-147-499-7310	Sequence 7310, Ap
279	6	5.0	74	24	US-60-197-873-23197	Sequence 23197, A	352	6	5.0	98	24	US-60-177-571-4859	Sequence 4859, Ap
280	6	5.0	74	28	US-09-621-976-6396	Sequence 6396, Ap	353	6	5.0	98	24	US-60-182-467-2130	Sequence 2130, Ap
281	6	5.0	75	1	PCT-US01-01354-18745	Sequence 18745, A	354	6	5.0	98	28	US-09-621-976-7310	Sequence 7310, Ap
282	6	5.0	75	21	US-09-758-456-347	Sequence 347, App	355	6	5.0	99	15	US-09-134-000-6615	Sequence 6615, Ap
283	6	5.0	75	21	US-09-764-905-18745	Sequence 18745, A	356	6	5.0	99	27	US-09-708-427-45215	Sequence 45215, A
284	6	5.0	75	24	US-60-182-568-925	Sequence 925, App	357	6	5.0	99	27	US-09-708-427-73343	Sequence 73343, A
285	6	5.0	76	26	US-10-092-399-18745	Sequence 18745, A	358	6	5.0	100	1	PCT-US01-08631-38558	Sequence 38558, A
286	6	5.0	76	22	US-09-854-847-12	Sequence 12, Appl	359	6	5.0	100	27	US-09-675-784A-7681	Sequence 7681, Ap
287	6	5.0	76	24	US-60-196-712-2749	Sequence 2749, Ap	360	6	5.0	101	24	US-60-104-346-12	Sequence 12, Appl
288	6	5.0	78	17	US-09-674-266A-317	Sequence 317, App	361	6	5.0	101	24	US-60-170-374-2619	Sequence 2619, Ap
289	6	5.0	79	17	US-09-330-781-354	Sequence 354, App	362	6	5.0	101	24	US-60-182-467-2129	Sequence 2129, Ap
290	6	5.0	79	22	US-09-828-769-354	Sequence 354, App	363	6	5.0	102	11	US-08-779-828-23	Sequence 23, Appl
291	6	5.0	79	24	US-60-311-261-1585	Sequence 1585, Ap	364	6	5.0	102	11	US-08-780-890-23	Sequence 23, Appl
292	6	5.0	79	27	US-09-708-427-81180	Sequence 81180, A	365	6	5.0	102	12	US-08-864-572-23	Sequence 23, Appl
293	6	5.0	80	20	US-09-617-682A-4181	Sequence 4181, Ap	366	6	5.0	102	21	US-09-758-442-430	Sequence 430, App

367	6	5.0	103	22	US-09-834-366-17345	Sequence 17345, A	440	6	5.0	129	24	US-60-169-868-5923	Sequence 5923, Ap
368	6	5.0	103	24	US-60-197-873-17345	Sequence 17345, A	441	6	5.0	129	24	US-60-178-306-1368	Sequence 1368, Ap
369	6	5.0	104	19	US-09-539-697-68	Sequence 68, Appl	442	6	5.0	130	27	US-09-708-427-46500	Sequence 46500, A
370	6	5.0	104	27	US-09-965-602-68	Sequence 68, Appl	443	6	5.0	130	27	US-09-708-427-73891	Sequence 73891, A
371	6	5.0	104	27	US-09-620-111B-7352	Sequence 7352, Ap	444	6	5.0	131	21	US-09-733-089-16723	Sequence 16723, A
372	6	5.0	105	1	PCT-US00-26524B-8420	Sequence 8420, Ap	445	6	5.0	131	22	US-09-816-660-16723	Sequence 16723, A
373	6	5.0	105	21	US-09-758-471-4440	Sequence 4440, Ap	446	6	5.0	132	24	US-60-147-189-902	Sequence 902, App
374	6	5.0	105	22	US-09-834-366-16497	Sequence 16497, A	447	6	5.0	133	16	US-09-270-767-32096	Sequence 32096, A
375	6	5.0	105	24	US-60-197-873-16497	Sequence 16497, A	448	6	5.0	133	24	US-60-169-841-1781	Sequence 1781, Ap
376	6	5.0	106	1	PCT-US00-06782-122	Sequence 122, App	449	6	5.0	134	21	US-09-735-004-4	Sequence 4, Appl1
377	6	5.0	106	20	US-09-688-052-3827	Sequence 3827, Ap	450	6	5.0	134	24	US-60-139-669-484	Sequence 484, App
378	6	5.0	106	21	US-09-758-447-762	Sequence 762, App	451	6	5.0	136	17	US-09-325-932-76	Sequence 76, Appl
379	6	5.0	107	11	US-08-728-742-9	Sequence 9, Appl1	452	6	5.0	136	17	US-09-325-932A-76	Sequence 76, Appl
380	6	5.0	107	11	US-08-728-742A-9	Sequence 9, Appl1	453	6	5.0	136	17	US-09-327-373-76	Sequence 76, Appl
381	6	5.0	107	16	US-09-252-691-10101	Sequence 10101, A	454	6	5.0	137	15	US-09-134-000-5195	Sequence 5195, Ap
382	6	5.0	107	16	US-09-252-691C-10101	Sequence 10101, A	455	6	5.0	137	15	US-09-134-000-5195	Sequence 5195, Ap
383	6	5.0	107	18	US-09-417-507-25236	Sequence 25236, A	456	6	5.0	137	27	US-09-977-418-36	Sequence 36, Appl
384	6	5.0	109	16	US-09-767-47313	Sequence 47313, A	457	6	5.0	137	28	US-09-977-033A-36	Sequence 36, Appl
385	6	5.0	109	16	US-09-270-849B-182881	Sequence 182881, A	458	6	5.0	138	23	US-09-902-540-11211	Sequence 11211, A
386	6	5.0	110	17	US-09-325-932-77	Sequence 77, Appl	459	6	5.0	139	1	PCT-US97-04115-66	Sequence 66, Appl
387	6	5.0	110	17	US-09-325-932A-77	Sequence 77, Appl	460	6	5.0	139	20	US-09-614-450-2555	Sequence 2555, Ap
388	6	5.0	110	17	US-09-327-373-77	Sequence 77, Appl	461	6	5.0	139	27	US-09-399-118-66	Sequence 66, Appl
389	6	5.0	110	17	US-09-733-089-9219	Sequence 9219, Ap	462	6	5.0	140	24	US-60-186-281-316	Sequence 316, App
390	6	5.0	110	22	US-09-816-660-9219	Sequence 9219, Ap	463	6	5.0	141	1	PCT-US01-08631-42228	Sequence 42228, A
391	6	5.0	111	1	PCT-US01-01324-1408	Sequence 1408, Ap	464	6	5.0	141	1	PCT-US01-08631-42228	Sequence 42228, A
392	6	5.0	111	26	US-10-079-979-1408	Sequence 1408, Ap	465	6	5.0	141	18	US-09-417-507-27719	Sequence 27719, A
393	6	5.0	112	22	US-09-834-366-15953	Sequence 15953, A	466	6	5.0	141	24	US-60-178-306-1367	Sequence 1367, Ap
394	6	5.0	112	22	US-09-834-366-17543	Sequence 17543, A	467	6	5.0	141	25	US-60-361-742-612	Sequence 612, App
395	6	5.0	112	24	US-60-197-873-15953	Sequence 15953, A	468	6	5.0	142	24	US-60-196-713-3486	Sequence 3486, Ap
396	6	5.0	112	24	US-60-197-873-17543	Sequence 17543, A	469	6	5.0	143	16	US-09-252-691-8747	Sequence 8747, Ap
397	6	5.0	113	1	PCT-US01-01338-1547	Sequence 1547, Ap	470	6	5.0	143	16	US-08-252-691C-8747	Sequence 8747, Ap
398	6	5.0	113	1	PCT-US01-01359-98	Sequence 98, Appl	471	6	5.0	143	21	US-09-733-089-9199	Sequence 9199, Ap
399	6	5.0	113	21	US-09-764-863-98	Sequence 98, Appl	472	6	5.0	143	22	US-09-803-110-12748	Sequence 12748, A
400	6	5.0	113	21	US-09-764-877-1547	Sequence 1547, Ap	473	6	5.0	143	24	US-60-170-346-1550	Sequence 1550, Ap
401	6	5.0	113	24	US-60-213-178-663	Sequence 663, App	474	6	5.0	144	1	PCT-US00-05881-795	Sequence 795, App
402	6	5.0	113	27	US-09-989-442-98	Sequence 98, Appl	475	6	5.0	144	23	US-09-925-298-795	Sequence 795, App
403	6	5.0	113	27	US-09-708-427-73892	Sequence 73892, A	476	6	5.0	144	24	US-60-173-465-352	Sequence 352, App
404	6	5.0	114	1	PCT-US01-00663-36257	Sequence 36257, A	477	6	5.0	146	16	US-09-248-796-26049	Sequence 26049, A
405	6	5.0	114	22	US-09-864-761-41031	Sequence 41031, A	478	6	5.0	146	27	US-09-620-111B-7350	Sequence 7350, Ap
406	6	5.0	114	26	US-10-023-386-34154	Sequence 34154, A	479	6	5.0	148	27	US-09-708-427-63259	Sequence 63259, A
407	6	5.0	114	27	US-09-828-708-11	Sequence 11, Appl	480	6	5.0	149	24	US-60-312-544-10721	Sequence 10721, A
408	6	5.0	114	27	US-09-675-784A-13357	Sequence 13357, A	481	6	5.0	150	21	US-09-733-089-9199	Sequence 9199, Ap
409	6	5.0	115	27	US-09-675-784A-9630	Sequence 9630, Ap	482	6	5.0	150	22	US-09-816-660-9199	Sequence 9199, Ap
410	6	5.0	116	1	PCT-US97-07950-403	Sequence 403, App	483	6	5.0	150	24	US-60-171-434-1489	Sequence 1489, Ap
411	6	5.0	116	12	US-08-858-207A-403	Sequence 403, App	484	6	5.0	150	27	US-09-611-526-3409	Sequence 3409, Ap
412	6	5.0	118	15	US-09-127-238-16	Sequence 16, Appl	485	6	5.0	151	27	US-09-708-427-37421	Sequence 37421, A
413	6	5.0	118	21	US-09-758-461-677	Sequence 677, App	486	6	5.0	152	24	US-60-140-806-903	Sequence 903, App
414	6	5.0	118	21	US-09-760-469-1093	Sequence 1093, Ap	487	6	5.0	153	21	US-09-700-708-4	Sequence 4, Appl1
415	6	5.0	122	1	PCT-US01-00911-356	Sequence 256, App	488	6	5.0	153	21	US-09-758-472-5508	Sequence 5508, Ap
416	6	5.0	122	1	PCT-US01-29871-259	Sequence 259, App	489	6	5.0	153	28	US-09-455-978B-76	Sequence 76, Appl
417	6	5.0	122	1	PCT-US99-15849-251	Sequence 251, App	490	6	5.0	154	16	US-09-252-931A-24585	Sequence 24585, A
418	6	5.0	122	18	US-09-482-273-256	Sequence 256, App	491	6	5.0	154	24	US-09-732-210-859	Sequence 859, App
419	6	5.0	122	27	US-09-620-111B-7351	Sequence 7351, Ap	492	6	5.0	154	24	US-60-169-340-859	Sequence 859, App
420	6	5.0	122	27	US-09-984-276-256	Sequence 256, App	493	6	5.0	155	24	US-60-173-462-62	Sequence 62, Appl
421	6	5.0	122	27	US-09-984-271-256	Sequence 256, App	494	6	5.0	155	27	US-09-708-427-79365	Sequence 79365, A
422	6	5.0	123	20	US-09-614-450-2557	Sequence 2557, Ap	495	6	5.0	156	19	US-09-583-110-5095	Sequence 5095, Ap
423	6	5.0	123	27	US-09-708-427-79794	Sequence 79794, A	496	6	5.0	156	22	US-09-833-730-252	Sequence 252, App
424	6	5.0	124	21	US-09-758-445-610	Sequence 610, App	497	6	5.0	156	24	US-60-207-362-42	Sequence 14, Appl
425	6	5.0	124	26	US-10-015-127-13943	Sequence 13943, A	498	6	5.0	156	27	US-09-708-427-55194	Sequence 55194, A
426	6	5.0	125	1	PCT-US97-09911-34	Sequence 34, Appl	499	6	5.0	156	27	US-09-708-427-78835	Sequence 78835, A
427	6	5.0	125	1	PCT-US98-25247-317	Sequence 317, App	500	6	5.0	156	28	US-09-769-787-98	Sequence 98, Appl
428	6	5.0	125	1	PCT-US98-25247-317	Sequence 317, App	501	6	5.0	157	1	PCT-US99-05485-19	Sequence 19, Appl
429	6	5.0	125	15	US-09-193-637-317	Sequence 317, App	502	6	5.0	157	16	US-09-270-767-33788	Sequence 33788, A
430	6	5.0	125	15	US-09-193-637A-317	Sequence 317, App	503	6	5.0	157	16	US-09-270-767-49005	Sequence 49005, A
431	6	5.0	125	28	US-09-975-719-317	Sequence 317, App	504	6	5.0	157	16	US-09-270-767-49005	Sequence 49005, A
432	6	5.0	127	1	PCT-US00-06112-715	Sequence 715, App	505	6	5.0	157	16	US-09-758-450-759	Sequence 759, App
433	6	5.0	127	20	US-09-640-211A-715	Sequence 715, App	506	6	5.0	157	21	US-09-758-450-759	Sequence 759, App
434	6	5.0	127	27	US-09-708-427-79793	Sequence 79793, A	507	6	5.0	157	24	US-60-181-328-19	Sequence 19, Appl
435	6	5.0	128	1	PCT-US01-08631-44231	Sequence 44231, A	508	6	5.0	158	1	PCT-US01-08631-42038	Sequence 42038, A
436	6	5.0	128	1	PCT-US01-08631-47130	Sequence 47130, A	509	6	5.0	158	18	US-09-417-507-23780	Sequence 23780, A
437	6	5.0	129	12	US-08-864-517-2	Sequence 2, Appl1	510	6	5.0	158	22	US-09-834-366-14169	Sequence 14169, A
438	6	5.0	129	19	US-09-502-967-36	Sequence 36, Appl	511	6	5.0	158	24	US-60-197-873-14169	Sequence 14169, A
439	6	5.0	129	24	US-60-160-209-4028	Sequence 4028, Ap	512	6	5.0	159	28	US-09-628-987B-993	Sequence 993, App

513	6	5.0	160	21	US-09-758-449-868	Sequence 868, App	586	199	27	US-09-708-427-1659	Sequence 1659, Ap
514	6	5.0	161	15	US-09-134-000-3821	Sequence 3821, Ap	587	199	27	US-09-708-427-17227	Sequence 17227, A
515	6	5.0	161	27	US-09-620-111B-4580	Sequence 4580, Ap	588	200	21	US-09-758-472-9531	Sequence 9531, Ap
516	6	5.0	161	32	PCT-US02-05109-744	Sequence 744, App	589	200	24	US-60-248-505-683	Sequence 683, App
517	6	5.0	162	18	US-09-417-507-23339	Sequence 23339, A	590	200	24	US-09-620-394B-1021	Sequence 1021, Ap
518	6	5.0	163	24	US-60-233-939-146	Sequence 146, App	591	202	1	PCT-US01-08631-41521	Sequence 41521, A
519	6	5.0	164	15	US-09-121-238-45	Sequence 45, Appl	592	202	21	US-09-760-469-1062	Sequence 1062, Ap
520	6	5.0	164	24	US-60-261-976-260	Sequence 260, App	593	202	24	US-09-760-469-1062	Sequence 1104, Ap
521	6	5.0	165	24	US-60-162-356-704	Sequence 704, App	594	203	24	US-60-248-505-1104	Sequence 1104, Ap
522	6	5.0	165	24	US-60-169-842-3898	Sequence 3898, Ap	595	203	24	US-60-324-631-1358	Sequence 1358, Ap
523	6	5.0	166	1	PCT-US00-12788-450	Sequence 450, App	596	204	9	US-08-561-963-16	Sequence 16, Appl
524	6	5.0	166	22	US-09-864-761-47670	Sequence 47670, A	597	204	20	US-09-692-059-16	Sequence 16, Appl
525	6	5.0	166	24	US-60-236-359-20531	Sequence 20531, A	598	204	24	US-60-162-245-4110	Sequence 4110, Ap
526	6	5.0	166	27	US-09-986-480-450	Sequence 450, App	599	204	24	US-60-169-868-6848	Sequence 6848, Ap
527	6	5.0	167	12	US-08-827-356-5464	Sequence 5464, Ap	600	205	16	US-09-270-767-39126	Sequence 39126, A
528	6	5.0	167	20	US-09-611-529-6982	Sequence 6982, Ap	601	205	16	US-09-270-767-54343	Sequence 54343, A
529	6	5.0	168	24	US-60-167-217-16598	Sequence 16598, A	602	205	16	US-09-270-849B-190584	Sequence 190584, A
530	6	5.0	168	24	US-60-191-637-16607	Sequence 16607, A	603	205	27	PCT-US09-708-427-69912	Sequence 69912, A
531	6	5.0	168	27	US-09-614-150-16563	Sequence 16563, A	604	206	1	PCT-US00-34004-4	Sequence 4, Appli
532	6	5.0	169	24	US-60-138-684-917	Sequence 917, App	605	206	18	US-09-467-870-4	Sequence 4, Appli
533	6	5.0	171	21	US-09-760-469-1026	Sequence 1026, Ap	606	207	21	US-09-733-089-5331	Sequence 5331, Ap
534	6	5.0	172	16	US-09-270-767-60977	Sequence 60977, A	607	208	19	US-09-816-660-5331	Sequence 5331, Ap
535	6	5.0	172	16	US-09-270-849B-191535	Sequence 191535, A	608	208	19	US-09-570-581A-1519	Sequence 1519, Ap
536	6	5.0	173	24	US-60-167-217-9676	Sequence 9676, Ap	609	208	19	US-09-573-655A-31	Sequence 31, Appl
537	6	5.0	173	27	US-60-191-637-9662	Sequence 9662, Ap	610	209	1	PCT-US01-03800A-2610	Sequence 2610, Ap
538	6	5.0	173	27	US-09-614-150-9630	Sequence 9630, Ap	611	209	24	US-60-167-217-10518	Sequence 10518, A
539	6	5.0	175	1	PCT-US97-02318-603	Sequence 603, App	612	209	24	US-60-173-464-8494	Sequence 8494, Ap
540	6	5.0	175	13	US-08-903-470-603	Sequence 603, App	613	209	24	US-60-191-637-10529	Sequence 10529, A
541	6	5.0	175	15	US-09-107-433-2630	Sequence 2630, Ap	614	209	24	US-60-191-681-8231	Sequence 8231, Ap
542	6	5.0	175	28	US-09-628-987B-992	Sequence 992, App	615	209	27	US-09-708-427-70387	Sequence 70387, A
543	6	5.0	177	6	US-08-284-667A-24	Sequence 24, Appl	616	209	27	US-09-614-150-10497	Sequence 10497, A
544	6	5.0	177	10	US-08-671-548-24	Sequence 24, Appl	617	210	13	US-08-933-750-6	Sequence 6, Appli
545	6	5.0	177	10	US-08-671-548A-24	Sequence 24, Appl	618	210	16	US-09-209-533-4	Sequence 4, Appli
546	6	5.0	177	10	US-08-671-548C-24	Sequence 24, Appl	619	210	16	US-09-252-991A-28014	Sequence 28014, A
547	6	5.0	178	4	US-08-053-863-37	Sequence 37, Appl	620	210	19	US-09-518-865-6	Sequence 6, Appli
548	6	5.0	180	27	US-09-620-394B-1022	Sequence 1022, Ap	621	210	21	US-09-739-449-9889	Sequence 9889, Ap
549	6	5.0	182	21	US-09-758-472-5634	Sequence 5634, Ap	622	210	22	US-09-803-110-9889	Sequence 9889, Ap
550	6	5.0	183	16	US-09-201-228A-113	Sequence 113, App	623	210	22	US-09-840-787-6	Sequence 6, Appli
551	6	5.0	184	16	US-08-252-991A-32916	Sequence 32916, A	624	210	24	US-60-145-138-714	Sequence 714, App
552	6	5.0	185	21	US-09-757-027-679	Sequence 679, App	625	210	28	US-09-690-196-4	Sequence 4, Appli
553	6	5.0	185	21	US-09-760-475-2531	Sequence 2531, Ap	626	211	19	US-09-596-746-48	Sequence 48, Appl
554	6	5.0	185	23	US-09-902-540-14546	Sequence 14546, A	627	211	24	US-60-311-261-1632	Sequence 1632, Ap
555	6	5.0	186	18	US-09-417-507-34593	Sequence 34593, A	628	212	1	PCT-US94-13540-4	Sequence 4, Appli
556	6	5.0	187	21	US-09-738-626-4821	Sequence 4821, Ap	629	212	11	US-08-753-159-4	Sequence 4, Appli
557	6	5.0	187	21	US-09-606-740A-774	Sequence 774, App	630	212	15	US-09-180-089-7	Sequence 7, Appli
558	6	5.0	188	16	US-09-248-796-14402	Sequence 14402, A	631	212	18	US-09-488-725A-3333	Sequence 3333, Ap
559	6	5.0	191	27	US-09-708-427-1660	Sequence 1660, Ap	632	212	19	US-09-570-186-4	Sequence 4, Appli
560	6	5.0	191	27	US-09-708-427-17044	Sequence 17044, A	633	212	19	US-09-596-746A-48	Sequence 48, Appl
561	6	5.0	191	27	US-09-594-595B-503	Sequence 503, App	634	212	21	US-09-711-546-11	Sequence 11, Appl
562	6	5.0	192	16	US-09-270-767-38171	Sequence 38171, A	635	212	23	US-09-944-807-8	Sequence 8, Appli
563	6	5.0	192	16	US-09-270-767-53388	Sequence 53388, A	636	212	27	US-09-974-992-7	Sequence 7, Appli
564	6	5.0	192	16	US-09-270-849B-188623	Sequence 188623, A	637	213	23	US-09-902-540-10588	Sequence 10588, A
565	6	5.0	193	1	PCT-US00-34004-6	Sequence 6, Appli	638	216	1	PCT-US01-08631-31047	Sequence 31047, A
566	6	5.0	193	18	US-09-467-870-6	Sequence 6, Appli	639	216	16	US-09-252-991A-26661	Sequence 26661, A
567	6	5.0	193	21	US-09-733-089-19703	Sequence 19703, A	640	216	18	US-09-489-039A-13568	Sequence 13568, A
568	6	5.0	193	21	US-09-733-089-19756	Sequence 19756, A	641	216	24	US-60-146-055-561	Sequence 561, App
569	6	5.0	193	22	US-09-816-660-19703	Sequence 19703, A	642	216	24	US-60-213-177-603	Sequence 603, App
570	6	5.0	193	22	US-09-816-660-19756	Sequence 19756, A	643	218	27	US-09-708-427-17043	Sequence 17043, A
571	6	5.0	194	6	US-08-284-667A-26	Sequence 26, Appl	644	219	19	US-09-540-236-3745	Sequence 3745, Ap
572	6	5.0	194	10	US-08-671-548-26	Sequence 26, Appl	645	219	24	US-60-128-476-3341	Sequence 3341, Ap
573	6	5.0	194	10	US-08-671-548A-26	Sequence 26, Appl	646	220	27	US-09-594-595B-502	Sequence 502, App
574	6	5.0	194	10	US-08-671-548C-26	Sequence 26, Appl	647	220	27	US-09-589-733-1	Sequence 1, Appli
575	6	5.0	195	16	US-09-248-796-14451	Sequence 14451, A	648	223	19	US-09-589-733-13	Sequence 13, Appl
576	6	5.0	195	16	US-09-248-796-19374	Sequence 19374, A	649	223	32	PCT-US01-27760-717	Sequence 717, App
577	6	5.0	196	24	US-60-324-109-31938	Sequence 31938, A	650	223	32	PCT-US01-27760A-717	Sequence 717, App
578	6	5.0	197	24	US-60-167-217-2334	Sequence 2334, Ap	651	225	24	US-09-708-427-70386	Sequence 70386, A
579	6	5.0	197	24	US-60-173-464-1896	Sequence 1896, Ap	652	225	24	US-60-261-976-287	Sequence 287, App
580	6	5.0	197	27	US-09-708-427-2111	Sequence 2111, Ap	653	225	27	US-09-594-595B-755	Sequence 755, App
581	6	5.0	197	27	US-09-708-427-36155	Sequence 36155, A	654	226	1	PCT-US01-08631-51664	Sequence 51664, A
582	6	5.0	197	27	US-09-708-427-55193	Sequence 55193, A	655	226	24	US-60-312-544-10247	Sequence 10247, A
583	6	5.0	197	27	US-09-708-427-78834	Sequence 78834, A	656	226	27	US-09-605-703B-1140	Sequence 1140, Ap
584	6	5.0	199	24	US-60-195-053-2659	Sequence 2659, Ap	657	227	27	US-09-708-427-27167	Sequence 27167, A
585	6	5.0	199	24	US-60-324-109-31805	Sequence 31805, A	658	228	23	US-09-417-507-23397	Sequence 23397, A
								228	23	US-09-902-540-16049	Sequence 16049, A

659	6	5.0	229	16	US-09-270-767-44085	Sequence 44085, A	732	6	5.0	244	27	US-09-897-516-6687	Sequence 6687, Ap
660	6	5.0	229	18	US-09-428-944-871	Sequence 871, App	733	6	5.0	245	1	PCT-US99-09034-38	Sequence 38, Appl
661	6	5.0	229	27	US-09-675-784A-8532	Sequence 8532, Ap	734	6	5.0	245	18	US-09-488-725A-6814	Sequence 6814, Ap
662	6	5.0	231	12	US-08-808-031-32	Sequence 32, Appl	735	6	5.0	246	24	US-60-248-798-206	Sequence 206, App
663	6	5.0	231	12	US-08-808-031A-34	Sequence 34, Appl	736	6	5.0	246	27	US-09-708-427-5592	Sequence 5592, A
664	6	5.0	232	1	PCT-US01-08631-57050	Sequence 57050, A	737	6	5.0	247	1	PCT-US00-28664A-57	Sequence 57, Appl
665	6	5.0	233	16	US-09-252-991A-23516	Sequence 23516, A	738	6	5.0	247	19	US-09-573-655A-977	Sequence 977, App
666	6	5.0	233	23	US-09-948-941-491	Sequence 491, App	739	6	5.0	247	22	US-09-832-129-57	Sequence 57, Appl
667	6	5.0	233	27	US-09-675-784A-10554	Sequence 10554, A	740	6	5.0	248	18	US-09-417-507-38933	Sequence 38933, A
668	6	5.0	234	23	US-08-902-540-12262	Sequence 12262, A	741	6	5.0	249	16	US-09-248-796-26797	Sequence 26797, A
669	6	5.0	235	1	PCT-US00-34004-2	Sequence 2, Appl	742	6	5.0	250	26	US-10-015-127-10552	Sequence 10552, A
670	6	5.0	235	1	PCT-US99-05993-2	Sequence 2, Appl	743	6	5.0	250	27	US-09-675-784A-11207	Sequence 11207, A
671	6	5.0	235	14	US-09-001-403-27	Sequence 27, Appl	744	6	5.0	250	27	US-09-594-595B-754	Sequence 754, App
672	6	5.0	235	14	US-09-046-316-2	Sequence 2, Appl	745	6	5.0	252	16	US-09-252-691C-11180	Sequence 11180, A
673	6	5.0	235	15	US-09-167-513-2	Sequence 2, Appl	746	6	5.0	252	16	US-09-252-691C-11180	Sequence 11180, A
674	6	5.0	235	16	US-09-247-155-95	Sequence 95, Appl	747	6	5.0	252	16	US-09-489-039A-10463	Sequence 10463, A
675	6	5.0	235	16	US-09-254-311-99	Sequence 99, Appl	748	6	5.0	253	16	US-09-248-796-27637	Sequence 27637, A
676	6	5.0	235	18	US-09-467-870-2	Sequence 2, Appl	749	6	5.0	253	27	US-09-605-703B-1138	Sequence 1138, Ap
677	6	5.0	235	18	US-09-469-099-14	Sequence 14, Appl	750	6	5.0	255	16	US-09-248-796-18600	Sequence 18600, A
678	6	5.0	235	21	US-09-702-114A-2	Sequence 2, Appl	751	6	5.0	258	1	PCT-US01-08631-35889	Sequence 35889, A
679	6	5.0	235	22	US-09-866-028-91	Sequence 91, Appl	752	6	5.0	259	1	PCT-US01-08631-57684	Sequence 57684, A
680	6	5.0	235	23	US-09-943-664-91	Sequence 91, Appl	753	6	5.0	259	1	PCT-US01-14827-13280	Sequence 13280, A
681	6	5.0	235	23	US-09-943-762-91	Sequence 91, Appl	754	6	5.0	259	1	PCT-US99-05721-122	Sequence 122, App
682	6	5.0	235	23	US-09-943-780-91	Sequence 91, Appl	755	6	5.0	259	17	US-09-393-022-127	Sequence 127, App
683	6	5.0	235	23	US-09-943-851-91	Sequence 91, Appl	756	6	5.0	259	27	US-09-798-889-127	Sequence 127, App
684	6	5.0	235	23	US-09-944-403-91	Sequence 91, Appl	757	6	5.0	260	19	US-09-543-681A-8210	Sequence 8210, Ap
685	6	5.0	235	23	US-09-944-413-91	Sequence 91, Appl	758	6	5.0	260	24	US-60-245-225-319	Sequence 319, App
686	6	5.0	235	23	US-09-944-449-91	Sequence 91, Appl	759	6	5.0	260	24	US-60-258-250-95	Sequence 95, Appl
687	6	5.0	235	23	US-09-944-457-91	Sequence 91, Appl	760	6	5.0	260	27	US-09-708-427-70385	Sequence 70385, A
688	6	5.0	235	23	US-09-944-654-91	Sequence 91, Appl	761	6	5.0	261	1	PCT-US01-08631-35953	Sequence 35953, A
689	6	5.0	235	23	US-09-944-862-91	Sequence 91, Appl	762	6	5.0	261	14	US-09-050-739-145	Sequence 145, App
690	6	5.0	235	23	US-09-944-944-91	Sequence 91, Appl	763	6	5.0	261	14	US-09-246-191-145	Sequence 145, App
691	6	5.0	235	23	US-09-945-015-91	Sequence 91, Appl	764	6	5.0	261	21	US-09-791-171-145	Sequence 145, App
692	6	5.0	235	23	US-09-945-584-91	Sequence 91, Appl	765	6	5.0	261	27	US-09-943-443-145	Sequence 145, App
693	6	5.0	235	23	US-09-945-587-91	Sequence 91, Appl	766	6	5.0	261	28	US-09-804-980-145	Sequence 145, App
694	6	5.0	235	26	US-10-002-796-32	Sequence 32, Appl	767	6	5.0	262	1	PCT-US98-12076-31	Sequence 31, Appl
695	6	5.0	235	26	US-10-028-072-390	Sequence 390, App	768	6	5.0	262	14	US-09-096-287-31	Sequence 31, Appl
696	6	5.0	235	26	US-10-066-193-32	Sequence 32, Appl	769	6	5.0	262	18	US-09-417-507-28482	Sequence 28482, A
697	6	5.0	235	26	US-10-066-198-32	Sequence 32, Appl	770	6	5.0	262	18	US-09-488-725A-2018	Sequence 2018, Ap
698	6	5.0	235	26	US-10-066-211-32	Sequence 32, Appl	771	6	5.0	262	21	US-09-746-783-65	Sequence 65, Appl
699	6	5.0	235	26	US-10-066-269-32	Sequence 32, Appl	772	6	5.0	265	1	PCT-US98-25247-57	Sequence 57, Appl
700	6	5.0	235	26	US-10-066-273-32	Sequence 32, Appl	773	6	5.0	265	1	PCT-US98-25247-57	Sequence 57, Appl
701	6	5.0	235	26	US-10-066-500-32	Sequence 32, Appl	774	6	5.0	265	15	US-09-199-637-57	Sequence 57, Appl
702	6	5.0	235	26	US-10-081-036-68	Sequence 68, Appl	775	6	5.0	265	15	US-09-199-637A-57	Sequence 57, Appl
703	6	5.0	235	26	US-10-066-203-32	Sequence 32, Appl	776	6	5.0	265	20	US-09-644-095-2	Sequence 2, Appl
704	6	5.0	235	26	US-10-066-494-32	Sequence 32, Appl	777	6	5.0	265	20	US-09-644-095-4	Sequence 4, Appl
705	6	5.0	235	27	US-09-944-097-91	Sequence 91, Appl	778	6	5.0	265	26	US-10-072-851-12297	Sequence 12297, A
706	6	5.0	235	27	US-09-944-896-91	Sequence 91, Appl	779	6	5.0	265	26	US-10-072-851-12873	Sequence 12873, A
707	6	5.0	235	27	US-09-943-851A-91	Sequence 91, Appl	780	6	5.0	265	27	US-09-815-242-12297	Sequence 12297, A
708	6	5.0	235	27	US-09-944-852-91	Sequence 91, Appl	781	6	5.0	265	27	US-09-815-242-12873	Sequence 12873, A
709	6	5.0	235	27	US-09-944-929-91	Sequence 91, Appl	782	6	5.0	265	28	US-09-973-719-57	Sequence 57, Appl
710	6	5.0	235	27	US-09-944-884-91	Sequence 91, Appl	783	6	5.0	265	32	PCT-US02-03987-12297	Sequence 12297, A
711	6	5.0	235	27	US-09-944-807-91	Sequence 91, Appl	784	6	5.0	265	32	PCT-US02-03987-12873	Sequence 12873, A
712	6	5.0	235	27	US-09-599-360B-14	Sequence 14, Appl	785	6	5.0	266	19	US-09-583-110-3761	Sequence 3761, Ap
713	6	5.0	235	27	US-09-944-396-91	Sequence 91, Appl	786	6	5.0	266	19	US-09-675-784A-12878	Sequence 12878, A
714	6	5.0	235	27	US-09-944-432-91	Sequence 91, Appl	787	6	5.0	267	16	US-09-252-691-8178	Sequence 8178, Ap
715	6	5.0	236	15	US-09-134-000-4896	Sequence 4896, Ap	788	6	5.0	267	16	US-09-252-691C-8178	Sequence 8178, Ap
716	6	5.0	236	15	US-09-902-540-16750	Sequence 16750, A	789	6	5.0	268	18	US-09-417-507-41802	Sequence 41802, A
717	6	5.0	237	16	US-09-270-767-39303	Sequence 39303, A	790	6	5.0	268	26	US-10-029-386-33381	Sequence 33381, A
718	6	5.0	237	16	US-09-270-767-54520	Sequence 54520, A	791	6	5.0	268	25	US-60-339-453-348	Sequence 348, App
719	6	5.0	237	16	US-09-270-849B-190954	Sequence 190954, A	792	6	5.0	272	27	US-09-708-427-55051	Sequence 55051, A
720	6	5.0	238	21	US-09-758-442-536	Sequence 536, App	793	6	5.0	272	27	US-09-708-427-79742	Sequence 79742, A
721	6	5.0	239	21	US-09-758-465-706	Sequence 706, App	794	6	5.0	273	1	PCT-US00-29360-227	Sequence 227, App
722	6	5.0	239	27	US-09-801-368-300	Sequence 300, App	795	6	5.0	273	27	US-09-708-427-69911	Sequence 69911, A
723	6	5.0	239	27	US-09-487-558-300	Sequence 300, App	796	6	5.0	274	18	US-09-488-725A-5590	Sequence 5590, Ap
724	6	5.0	239	27	US-09-708-427-2976	Sequence 2976, Ap	797	6	5.0	275	16	US-09-270-767-57659	Sequence 57659, A
725	6	5.0	239	27	US-09-487-558B-300	Sequence 300, App	798	6	5.0	275	16	US-09-270-849B-182612	Sequence 182612, A
726	6	5.0	240	16	US-09-248-796-20213	Sequence 20213, A	799	6	5.0	276	12	US-08-846-762-7	Sequence 7, Appl
727	6	5.0	240	16	US-09-248-796-20213	Sequence 2, Appl	800	6	5.0	276	17	US-09-352-994A-7	Sequence 7, Appl
728	6	5.0	241	17	US-09-387-372-3	Sequence 387, A	801	6	5.0	276	17	US-09-352-994A-7	Sequence 7, Appl
729	6	5.0	242	15	US-09-248-796-14587	Sequence 14587, A	802	6	5.0	277	12	US-08-827-356-3603	Sequence 3603, Ap
730	6	5.0	243	15	US-09-167-513-18	Sequence 167, A	803	6	5.0	277	15	US-09-134-001C-5612	Sequence 5612, Ap
731	6	5.0	244	24	US-60-215-161-6687	Sequence 6687, Ap	804	6	5.0	277	18	US-09-450-969-7379	Sequence 7379, Ap

805	6	5.0	277	20	US-09-611-529-6978	Sequence 6378, Ap	878	6	5.0	315	12	US-08-802-233-91	Sequence 91, Appl
806	6	5.0	278	1	PCT-US01-08631-35887	Sequence 35887, A	879	6	5.0	315	16	US-09-252-991A-26703	Sequence 26703, A
807	6	5.0	279	21	US-09-738-626-4303	Sequence 4303, Ap	880	6	5.0	316	16	US-09-248-796-19060	Sequence 19060, A
808	6	5.0	279	24	US-60-324-631-1068	Sequence 1068, Ap	881	6	5.0	319	24	US-60-173-464-18854	Sequence 18854, A
809	6	5.0	279	1	PCT-US01-08631-47976	Sequence 47976, A	882	6	5.0	319	24	US-60-191-637-22979	Sequence 22979, A
810	6	5.0	279	21	US-09-757-026-392	Sequence 392, App	883	6	5.0	319	24	US-60-191-681-18125	Sequence 18125, A
811	6	5.0	280	1	PCT-US01-04098A-3750	Sequence 3750, Ap	884	6	5.0	319	27	US-09-614-150-22899	Sequence 22899, A
812	6	5.0	281	1	PCT-US01-08631-47074	Sequence 47074, A	885	6	5.0	320	1	PCT-US97-01072-61	Sequence 61, Appl
813	6	5.0	281	12	US-08-827-359-2810	Sequence 2810, Ap	886	6	5.0	320	1	PCT-US97-21783-102	Sequence 102, Appl
814	6	5.0	281	20	US-09-611-529-5278	Sequence 5278, Ap	887	6	5.0	320	1	PCT-US98-05809-61	Sequence 61, Appl
815	6	5.0	281	21	US-09-758-471-4470	Sequence 4470, Ap	888	6	5.0	320	17	US-09-308-825A-102	Sequence 102, App
816	6	5.0	281	21	US-09-248-796-17101	Sequence 17101, A	889	6	5.0	320	27	US-09-684-938-102	Sequence 102, App
817	6	5.0	283	1	PCT-US01-08631-37177	Sequence 37177, A	890	6	5.0	320	27	US-09-713-601A-61	Sequence 61, Appl
818	6	5.0	283	16	US-09-252-991A-24178	Sequence 24178, A	892	6	5.0	320	28	US-09-350-597-61	Sequence 61, Appl
819	6	5.0	283	24	US-60-167-217-512	Sequence 512, App	893	6	5.0	321	24	US-60-312-544-10720	Sequence 10720, A
820	6	5.0	284	1	US-60-245-227-51	Sequence 51, Appl	894	6	5.0	322	8	US-08-402-601A-89	Sequence 89, Appl
821	6	5.0	284	1	PCT-US01-08631-56920	Sequence 56920, A	894	6	5.0	322	9	US-08-520-946-89	Sequence 89, Appl
822	6	5.0	284	18	US-09-434-968-78	Sequence 78, Appl	895	6	5.0	322	12	US-08-802-233-89	Sequence 89, Appl
823	6	5.0	285	15	US-09-107-433-4223	Sequence 4223, Ap	896	6	5.0	322	12	US-09-417-507-43060	Sequence 43060, A
824	6	5.0	286	1	PCT-US01-08631-32802	Sequence 32802, A	897	6	5.0	323	1	PCT-US01-01239-1382	Sequence 1382, Ap
825	6	5.0	286	20	US-09-674-741-12	Sequence 12, Appl	898	6	5.0	323	21	US-09-764-902-1382	Sequence 1382, Ap
826	6	5.0	286	27	US-09-675-784A-10608	Sequence 10608, A	899	6	5.0	325	18	US-09-468-253A-16	Sequence 16, Appl
827	6	5.0	287	24	US-60-146-315-626	Sequence 626, App	900	6	5.0	325	21	US-09-738-626-6072	Sequence 6072, Ap
828	6	5.0	287	21	US-09-738-626-5463	Sequence 5463, Ap	901	6	5.0	325	21	US-09-760-476-1769	Sequence 1769, Ap
829	6	5.0	288	27	US-09-708-427-54802	Sequence 54802, A	902	6	5.0	327	1	PCT-US01-29871-149	Sequence 149, App
830	6	5.0	290	24	US-60-312-544-7885	Sequence 7885, Ap	903	6	5.0	327	32	PCT-US02-08123-1199	Sequence 1199, Ap
831	6	5.0	291	21	US-09-758-460-498	Sequence 498, App	904	6	5.0	327	32	PCT-US02-08124-501	Sequence 501, App
832	6	5.0	294	20	US-09-674-741-17	Sequence 17, Appl	905	6	5.0	327	32	PCT-US02-08276-374	Sequence 374, App
833	6	5.0	294	21	US-09-758-441-304	Sequence 304, App	906	6	5.0	327	32	PCT-US02-08277-790	Sequence 790, App
834	6	5.0	295	1	PCT-US01-14827-9723	Sequence 9723, App	907	6	5.0	328	1	PCT-US01-00911-148	Sequence 148, App
835	6	5.0	296	1	PCT-US00-05988-1231	Sequence 1231, Ap	908	6	5.0	328	1	PCT-US99-15849-148	Sequence 148, App
836	6	5.0	296	23	US-09-925-300-1231	Sequence 1231, Ap	909	6	5.0	328	18	US-09-482-273-148	Sequence 148, App
837	6	5.0	296	27	US-09-708-427-27166	Sequence 27166, A	910	6	5.0	328	19	US-09-513-597-2	Sequence 2, Appli
838	6	5.0	297	21	US-09-738-626-6303	Sequence 6303, Ap	911	6	5.0	328	27	US-09-984-276-148	Sequence 148, App
839	6	5.0	297	27	US-08-870-962-1	Sequence 1, Appli	912	6	5.0	328	27	US-09-984-271-148	Sequence 148, App
840	6	5.0	299	12	US-08-827-356-4535	Sequence 4535, Ap	913	6	5.0	329	24	US-60-245-241-147	Sequence 147, App
841	6	5.0	299	20	US-09-611-529-7221	Sequence 7221, Ap	914	6	5.0	329	24	US-60-258-016-39	Sequence 39, Appl
842	6	5.0	300	17	US-09-328-352-4146	Sequence 4146, Ap	915	6	5.0	330	21	US-09-738-626-6014	Sequence 6014, Ap
843	6	5.0	300	18	US-09-417-507-31692	Sequence 31692, A	916	6	5.0	331	1	PCT-US01-08631-41692	Sequence 41692, A
844	6	5.0	300	19	US-09-585-858-42	Sequence 42, Appl	917	6	5.0	331	27	US-09-708-427-55049	Sequence 55049, A
845	6	5.0	300	21	US-09-733-089-8995	Sequence 8995, Ap	918	6	5.0	331	27	US-09-708-427-79740	Sequence 79740, A
846	6	5.0	300	22	US-09-816-660-8995	Sequence 8995, Ap	919	6	5.0	332	1	PCT-US01-08631-32979	Sequence 32979, A
847	6	5.0	301	27	US-09-675-784A-7239	Sequence 7239, Ap	920	6	5.0	332	21	US-09-738-626-5809	Sequence 5809, Ap
848	6	5.0	303	9	US-08-561-963-13	Sequence 13, Appl	921	6	5.0	332	21	US-09-792-024-73	Sequence 73, Appl
849	6	5.0	303	20	US-09-692-059-13	Sequence 13, Appl	922	6	5.0	332	24	US-60-259-128-4703	Sequence 4703, Ap
850	6	5.0	304	24	US-60-145-988-159	Sequence 159, App	923	6	5.0	332	24	US-60-314-050-7021	Sequence 7021, Ap
851	6	5.0	305	1	PCT-US01-08631-43514	Sequence 43514, A	924	6	5.0	332	26	US-10-032-585-7021	Sequence 7021, Ap
852	6	5.0	305	18	US-09-417-507-34290	Sequence 34290, A	925	6	5.0	332	26	US-10-072-851-14965	Sequence 14965, A
853	6	5.0	305	21	US-09-739-449-10966	Sequence 10966, A	926	6	5.0	332	32	PCT-US02-03987-14965	Sequence 14965, A
854	6	5.0	305	22	US-09-803-110-10966	Sequence 10966, A	927	6	5.0	333	18	US-09-488-725A-7007	Sequence 7007, Ap
855	6	5.0	305	27	US-09-708-427-55050	Sequence 55050, A	928	6	5.0	333	21	US-09-771-161-147	Sequence 147, App
856	6	5.0	305	27	US-09-708-427-79741	Sequence 79741, A	929	6	5.0	333	21	US-09-771-161A-147	Sequence 147, App
857	6	5.0	306	1	PCT-US01-08631-39244	Sequence 39244, A	930	6	5.0	334	24	US-60-312-544-8280	Sequence 8280, Ap
858	6	5.0	306	27	US-09-708-427-54801	Sequence 54801, A	931	6	5.0	335	1	PCT-US01-08631-55216	Sequence 55216, A
859	6	5.0	310	8	US-08-402-601A-88	Sequence 88, Appl	932	6	5.0	335	19	US-09-538-092-811	Sequence 811, App
860	6	5.0	310	9	US-08-520-946-88	Sequence 88, Appl	933	6	5.0	335	27	US-09-182-616-4	Sequence 4, Appli
861	6	5.0	310	12	US-08-802-233-88	Sequence 88, Appl	934	6	5.0	335	27	US-09-378-261-4	Sequence 4, Appli
862	6	5.0	310	16	US-09-270-767-42373	Sequence 42373, A	935	6	5.0	336	21	US-09-760-476-1666	Sequence 1666, Ap
863	6	5.0	311	24	US-60-167-217-15862	Sequence 15862, A	936	6	5.0	336	21	US-09-760-479-689	Sequence 689, App
864	6	5.0	311	24	US-60-191-637-15866	Sequence 15866, A	937	6	5.0	336	21	US-09-760-479-895	Sequence 895, App
865	6	5.0	311	27	US-09-708-427-65444	Sequence 65444, A	938	6	5.0	336	27	US-09-708-427-2602	Sequence 2602, App
866	6	5.0	311	27	US-09-614-150-15822	Sequence 15822, A	939	6	5.0	336	27	US-09-675-784A-12132	Sequence 12132, A
867	6	5.0	312	18	US-09-486-334-4	Sequence 4, Appli	940	6	5.0	337	1	PCT-US00-15410A-9	Sequence 9, Appli
868	6	5.0	312	20	US-09-674-741-18	Sequence 18, Appl	941	6	5.0	337	1	PCT-US01-08117-20	Sequence 20, Appl
869	6	5.0	313	1	PCT-US01-08631-41524	Sequence 41524, A	942	6	5.0	337	24	US-60-188-986-20	Sequence 20, Appl
870	6	5.0	313	16	US-09-252-691-10495	Sequence 10495, A	943	6	5.0	337	24	US-09-585-645-9	Sequence 9, Appli
871	6	5.0	313	16	US-09-427-691C-10495	Sequence 10495, A	944	6	5.0	337	27	US-09-585-645-44	Sequence 44, Appl
872	6	5.0	313	24	US-60-142-896-1068	Sequence 1068, Ap	945	6	5.0	337	27	US-09-980-381-9	Sequence 9, Appli
873	6	5.0	314	16	US-09-252-991A-27537	Sequence 27537, A	946	6	5.0	337	28	US-09-980-381-44	Sequence 44, Appl
874	6	5.0	314	24	US-60-135-519-14	Sequence 14, Appl	947	6	5.0	337	28	US-09-758-463-1090	Sequence 1090, Ap
875	6	5.0	315	7	US-09-708-427-65443	Sequence 65443, A	948	6	5.0	338	21	US-10-072-851-13545	Sequence 13545, A
876	6	5.0	315	8	US-08-402-601A-91	Sequence 91, Appl	949	6	5.0	339	27	US-09-815-242-13545	Sequence 13545, A
877	6	5.0	315	9	US-08-520-946-91	Sequence 91, Appl	950	6	5.0	339	27		

951 6 5.0 339 32 PCT-US02-03987-13545
952 6 5.0 340 16 US-09-270-767-40453
953 6 5.0 340 16 US-09-270-767-55669
954 6 5.0 341 16 US-09-270-849B-193369
955 6 5.0 341 18 US-09-468-253A-14
956 6 5.0 342 1 PCT-US98-20775-123
957 6 5.0 342 5 US-08-100-486-3
958 6 5.0 342 16 US-09-281-976-125
959 6 5.0 342 18 US-09-489-039A-7552
960 6 5.0 343 27 US-09-708-427-54800
961 6 5.0 344 24 US-60-173-464-29246
962 6 5.0 345 24 US-60-173-464-441
963 6 5.0 345 24 US-60-191-637-534
964 6 5.0 345 24 US-60-191-637-38368
965 6 5.0 345 24 US-60-191-681-423
966 6 5.0 345 24 US-60-191-681-29752
967 6 5.0 345 27 US-09-708-427-6029
968 6 5.0 345 27 US-09-614-150-534
969 6 5.0 345 27 US-09-614-150-38742
970 6 5.0 346 27 US-09-708-427-6028
971 6 5.0 348 1 PCT-US99-11576-10
972 6 5.0 348 8 US-08-462-966-2
973 6 5.0 348 17 US-09-318-271-10
974 6 5.0 348 20 US-09-624-183-2
975 6 5.0 348 24 US-60-125-054-10
976 6 5.0 350 16 US-09-252-691-7362
977 6 5.0 350 16 US-09-252-691C-7362
978 6 5.0 350 21 US-09-760-469-1086
979 6 5.0 350 24 US-60-215-161-6420
980 6 5.0 350 27 US-09-897-516-6420
981 6 5.0 350 27 US-09-281-646A-9
982 6 5.0 350 27 US-09-708-427-65442
983 6 5.0 356 21 US-09-738-626-6651
984 6 5.0 356 27 US-09-708-427-7472
985 6 5.0 358 21 US-09-733-089-23892
986 6 5.0 358 22 US-09-816-660-23892
987 6 5.0 359 1 PCT-US94-08055-4
988 6 5.0 359 18 US-09-417-507-43054
989 6 5.0 359 19 US-09-595-335A-297
990 6 5.0 359 26 US-10-044-643-51
991 6 5.0 359 26 US-10-044-643-52
992 6 5.0 359 28 US-09-708-427-10316
993 6 5.0 359 28 US-09-966-871-81
994 6 5.0 360 13 US-08-993-002A-6956
995 6 5.0 360 26 US-10-072-851-11378
996 6 5.0 360 27 US-09-815-242-11378
997 6 5.0 360 32 PCT-US02-03987-11378
998 6 5.0 361 1 PCT-US01-08631-50939
999 6 5.0 361 21 US-09-733-089-21818
1000 6 5.0 361 22 US-09-816-660-21818

ALIGNMENTS

RESULT 1

US-09-152-060-85

; Sequence 85, Application US/09152060

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P4

; CURRENT APPLICATION NUMBER: US/09/152,060

; PRIOR FILING DATE: 1998-09-11

; CURRENT APPLICATION NUMBER: PCT/US98/04858

; EARLIER FILING DATE: 1998-03-12

; EARLIER APPLICATION NUMBER: 60/040,762

; EARLIER FILING DATE: 1997-03-14

; EARLIER APPLICATION NUMBER: 60/040,710

; EARLIER FILING DATE: 1997-03-14

; EARLIER APPLICATION NUMBER: 60/050,934

; EARLIER FILING DATE: 1997-05-30

; EARLIER APPLICATION NUMBER: 60/048,100

; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85

LENGTH: 121

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (67)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (89)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-152-060-85

Query Match 98.3%; Score 119; DB 15; Length 121;

Best Local Similarity 100.0%; Pred.No. 6.2e-112; Indels 0; Gaps 0;
Matches 121; Conservative 0; Mismatches 0;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPQEEVPGGSKRDPDLYQLLQRLFKSHSSLEGL 60

Db 1 MRIMLFTAILAFSLAQSGAVCKEPQEEVPGGSKRDPDLYQLLQRLFKSHSSLEGL 60

QY 61 LKALSOXSTDPEKSTPEKRDMDHDFVGMGKRSVQDPDPTDQNVNPSFGILKYPRA 120

Db 61 LKALSOXSTDPEKSTPEKRDMDHDFVGMGKRSVQDPDPTDQNVNPSFGILKYPRA 120

QY 121 E 121

Db 121 E 121

RESULT 2

US-09-852-659-85

; Sequence 85, Application US/09852659

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P4

; CURRENT APPLICATION NUMBER: US/09/852,659

; CURRENT FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 60/265,583

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/152,060

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: PCT/US98/04858

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/050,934

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,100

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,357

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/057,765

```
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659-85

Query Match          98.3%; Score 119; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.2e-112;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
    |||||||
Db 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
    |||||||
Qy 61 LKALSOXSTDPKESTSPEKRDHDFVCGMGKRSVQPSPTDVNQENVPFSGILKYPRA 120
    |||||||
Db 61 LKALSOXSTDPKESTSPEKRDHDFVCGMGKRSVQPSPTDVNQENVPFSGILKYPRA 120
    |||||||
Qy 121 E 121
Db 121 E 121

RESULT 4
US-09-853-161-85
; Sequence 85, Application US/09853161
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (67)
; SOFTWARE: PatentIn Ver. 2.0

; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659-85

Query Match          98.3%; Score 119; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.2e-112;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
    |||||||
Db 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
    |||||||
Qy 61 LKALSOXSTDPKESTSPEKRDHDFVCGMGKRSVQPSPTDVNQENVPFSGILKYPRA 120
    |||||||
Db 61 LKALSOXSTDPKESTSPEKRDHDFVCGMGKRSVQPSPTDVNQENVPFSGILKYPRA 120
    |||||||
Qy 121 E 121
Db 121 E 121

RESULT 3
US-09-852-797-85
; Sequence 85, Application US/09852797
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
```

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-853-161-85

Query Match 98.3%; Score 119; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.2e-112;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
QY 61 LKALSOXSTDPKESTSPEKRDHDFVGMGKRSVOPDPTDYNQENVPFSGILKYPPRA 120
DB 61 LKALSOXSTDPKESTSPEKRDHDFVGMGKRSVOPDPTDYNQENVPFSGILKYPPRA 120
QY 121 E 121
DB 121 E 121

RESULT 5
US-10-058-993-85
; Sequence 85, Application US/10058993
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any amino acid

; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-058-993-85

Query Match 98.3%; Score 119; DB 26; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.2e-112;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
QY 61 LKALSOXSTDPKESTSPEKRDHDFVGMGKRSVOPDPTDYNQENVPFSGILKYPPRA 120
DB 61 LKALSOXSTDPKESTSPEKRDHDFVGMGKRSVOPDPTDYNQENVPFSGILKYPPRA 120
QY 121 E 121
DB 121 E 121

RESULT 6
US-09-834-366-13657
; Sequence 13657, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13657
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18..-1
US-09-834-366-13657

Query Match 54.5%; Score 66; DB 22; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
QY 61 LKALSO 66
DB 61 LKALSO 66
RESULT 7
US-60-197-873-13657
; Sequence 13657, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

```
; FILE REFERENCE: 81.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/197.873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13657
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18..-1
US-60-197-873-13657

Query Match          54.5%; Score 66; DB 24; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||
Db 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||

Qy 61 LKALSQ 66
    |||
Db 61 LKALSQ 66

RESULT 8
US-09-086-078-2
; Sequence 2, Application US/09086078
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NEUROKININ B PRECURSORS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,078
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-086-078-2
```

```
Query Match          54.5%; Score 66; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||
Db 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||

Qy 61 LKALSQ 66
    |||
Db 61 LKALSQ 66

RESULT 9
US-09-111-901-2
; Sequence 2, Application US/09111901
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID
; APPLICANT: HASTINGS, GREGG
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,901
; FILING DATE: 08-JULY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97305215.2
; FILING DATE: 14-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-111-901-2

Query Match          54.5%; Score 66; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||
Db 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||

Qy 61 LKALSQ 66
    |||
Db 61 LKALSQ 66

RESULT 10
```

```
US-09-152-060-68
; Sequence 68, Application US/09152060
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-68
```

```
Query Match      54.5%; Score 66; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.le-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60
   |||||||
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60

QY 61 LKALSQ 66
   |||||
Db 61 LKALSQ 66

RESULT 11
US-09-852-659-68
; Sequence 68, Application US/09852659
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
```

```
Query Match      54.5%; Score 66; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.le-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60
   |||||||
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60

QY 61 LKALSQ 66
   |||||
Db 61 LKALSQ 66

RESULT 12
US-09-852-797-68
; Sequence 68, Application US/09852797
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659-68
```

```
Query Match      54.5%; Score 66; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.le-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60
   |||||||
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60

QY 61 LKALSQ 66
   |||||
Db 61 LKALSQ 66

RESULT 12
US-09-852-797-68
; Sequence 68, Application US/09852797
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-68
```

Query Match 54.5%; Score 66; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEEVPVGGGRKRPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEEVPVGGGRKRPDLYQLLQRLFKSHSLEGL 60

QY 61 LKALSQ 66
Db 61 LKALSQ 66

RESULT 13

US-09-853-161-68
; Sequence 68, Application US/09853161
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P3

; CURRENT APPLICATION NUMBER: US/09/853,161

; CURRENT FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 60/265,583

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/152,060

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: PCT/US98/04858

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/050,934

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,100

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,357

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/057,765

; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: 60/048,970

; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/068,368

; PRIOR FILING DATE: 1997-12-19

; NUMBER OF SEQ ID NOS: 118

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 68

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-853-161-68

Query Match 54.5%; Score 66; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEEVPVGGGRKRPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEEVPVGGGRKRPDLYQLLQRLFKSHSLEGL 60

QY 61 LKALSQ 66
Db 61 LKALSQ 66

RESULT 14

US-10-058-993-68

; Sequence 68, Application US/10058993

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P5

; CURRENT APPLICATION NUMBER: US/10/058,993

; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: 09/852,659

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 09/852,797

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 09/853,161

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 60/265,583

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/152,060

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: PCT/US98/04858

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/068,368

; PRIOR FILING DATE: 1997-12-19

; PRIOR APPLICATION NUMBER: 60/057,765

; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: 60/048,970

; PRIOR FILING DATE: 1997-06-05

; PRIOR APPLICATION NUMBER: 60/050,934

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,100

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,357

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/040,710

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 68

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-058-993-68

Query Match 54.5%; Score 66; DB 26; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEEVPVGGGRKRPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEEVPVGGGRKRPDLYQLLQRLFKSHSLEGL 60

QY 61 LKALSQ 66
Db 61 LKALSQ 66

RESULT 15

US-08-879-995-1

; Sequence 1, Application US/08879995

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Kaser, Matthew R.

; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995
FILING DATE: Herewith
CLASSIFICATION: ?
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-853-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT03
CLONE: 2109906
US-08-879-995-1

Query Match 54.5%; Score 66; DB 12; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRIMLLFTALFSLAQSGAVCKEPEQEEVYPGGGRKRPDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTALFSLAQSGAVCKEPEQEEVYPGGGRKRPDPDLYQLLQRLFKSHSLEGL 60
QY 61 LKALSQ 66
Db 61 LKALSQ 66

Search completed: May 3, 2002, 12:31:13
Job time: 230 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 16:38:52 ; Search time 8.51 Seconds
(without alignments)
167.521 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRTLFTALFSLAQSG.....DVNQNVPSGILKYPRAE 121

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 59194 seqs, 11781848 residues

Word size : 0

Total number of hits satisfying chosen parameters: 59194

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending Patents AA.New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	54.5	135	5	US-09-991-150-359
2	66	54.5	135	6	US-10-119-480-108
3	6	5.0	17	1	PCT-US02-10788-25
4	6	5.0	26	5	US-09-710-038A-30
5	6	5.0	26	6	US-10-043-074-19
6	6	5.0	63	6	US-10-103-295-163
7	6	5.0	84	5	US-09-540-209B-7680
8	6	5.0	96	5	US-09-990-004A-166
9	6	5.0	105	6	US-10-106-698-8430
10	6	5.0	110	5	US-09-990-004A-77
11	6	5.0	114	1	PCT-US02-10788-11
12	6	5.0	122	6	US-10-103-295-259
13	6	5.0	136	5	US-09-990-004A-76
14	6	5.0	138	5	US-09-540-209B-7831
15	6	5.0	144	6	US-10-102-806-795
16	6	5.0	168	5	US-09-988-915-2
17	6	5.0	192	5	US-09-540-209B-5932
18	6	5.0	208	5	US-09-573-655B-31
19	6	5.0	216	5	US-09-540-209B-5869
20	6	5.0	229	5	US-09-988-915-7
21	6	5.0	235	6	US-10-121-049-390
22	6	5.0	235	6	US-10-121-050-390
23	6	5.0	235	6	US-10-121-053-390
24	6	5.0	235	6	US-10-121-043-390
25	6	5.0	235	6	US-10-121-044-390
26	6	5.0	235	6	US-10-121-047-390
27	6	5.0	235	6	US-10-121-054-390
28	6	5.0	235	6	US-10-121-056-390
29	6	5.0	235	6	US-10-121-057-390
30	6	5.0	235	6	US-10-121-058-390
31	6	5.0	235	6	US-10-121-060-390
32	6	5.0	235	6	US-10-121-063-390
33	6	5.0	235	6	US-10-123-108-390
34	6	5.0	235	6	US-10-123-134-390
35	6	5.0	235	6	US-10-123-156-390
36	6	5.0	235	6	US-10-123-157-390
37	6	5.0	235	6	US-10-123-212-390
38	6	5.0	235	6	US-10-123-213-390
39	6	5.0	235	6	US-10-123-109-390
40	6	5.0	235	6	US-10-121-041-390
41	6	5.0	235	6	US-10-121-045-390
42	6	5.0	235	6	US-10-121-046-390
43	6	5.0	235	6	US-10-121-051-390
44	6	5.0	237	5	US-09-540-209B-5990
45	6	5.0	247	5	US-09-573-655B-977
46	6	5.0	327	1	PCT-US02-09785-657
47	6	5.0	327	6	US-10-103-295-149
48	6	5.0	375	5	US-09-895-913A-162
49	6	5.0	388	5	US-09-540-209B-6673
50	6	5.0	397	5	US-09-573-655B-1795
51	6	5.0	398	1	PCT-US02-07826-203
52	6	5.0	398	6	US-10-097-340-203
53	6	5.0	404	6	US-10-103-295-238
54	6	5.0	430	5	US-09-540-209B-6976
55	6	5.0	459	5	US-09-988-915-1
56	6	5.0	470	5	US-09-573-655B-2386
57	6	5.0	506	5	US-09-540-209B-5617
58	6	5.0	556	1	PCT-US02-10824-136
59	6	5.0	576	1	PCT-US02-07025-9
60	6	5.0	612	1	PCT-US02-07826-201
61	6	5.0	612	6	US-10-097-340-201
62	6	5.0	613	5	US-09-540-209B-7921
63	6	5.0	620	1	PCT-US02-07826-197
64	6	5.0	620	6	US-10-097-340-197
65	6	5.0	622	1	PCT-US02-07826-205
66	6	5.0	622	6	US-10-097-340-205
67	6	5.0	628	1	PCT-US02-07826-208
68	6	5.0	628	6	US-10-097-340-208
69	6	5.0	630	1	PCT-US02-07826-195
70	6	5.0	630	1	PCT-US02-07826-210
71	6	5.0	630	6	US-10-097-340-195
72	6	5.0	630	6	US-10-097-340-210
73	6	5.0	665	7	US-60-365-264-387
74	6	5.0	694	1	PCT-US02-07826-199
75	6	5.0	694	6	US-10-097-340-199
76	6	5.0	702	1	PCT-US02-07826-193
77	6	5.0	702	6	US-10-097-340-193
78	6	5.0	793	5	US-09-573-655B-1508
79	6	5.0	823	5	US-09-895-913A-244
80	6	5.0	1077	6	US-10-121-911-1
81	6	4.1	10	5	US-09-423-037A-6
82	5	4.1	11	1	PCT-US02-09534-132
83	5	4.1	11	5	US-09-423-037A-33
84	5	4.1	11	5	US-10-109-171-132
85	5	4.1	12	1	PCT-US02-09534-138
86	5	4.1	12	5	US-09-978-309A-37
87	5	4.1	12	6	US-10-109-171-138
88	5	4.1	15	1	PCT-US02-09534-43
89	5	4.1	15	1	PCT-US02-09534-152
90	5	4.1	15	6	US-10-109-171-43
91	5	4.1	15	6	US-10-109-171-152
92	5	4.1	22	6	US-10-105-299-4929
93	5	4.1	23	5	US-09-379-830A-20
94	5	4.1	24	1	PCT-US02-10764-14
95	5	4.1	24	1	PCT-US02-10764-27
96	5	4.1	29	1	PCT-US02-01109-82
97	5	4.1	31	6	US-10-105-299-4810
98	5	4.1	32	6	US-10-105-299-4646
99	5	4.1	33	1	PCT-US02-10764-37

100	5	4.1	36	6	US-10-105-299-5480	Sequence 5480, Ap	173	5	4.1	121	6	US-10-015-386A-354	Sequence 354, App
101	5	4.1	36	6	US-10-105-299-5858	Sequence 5858, Ap	174	5	4.1	121	6	US-10-015-387A-354	Sequence 354, App
102	5	4.1	36	6	US-10-106-698-8538	Sequence 8538, Ap	175	5	4.1	122	1	PCr-US02-09785-1014	Sequence 1014, Ap
103	5	4.1	38	6	US-10-100-679-67	Sequence 67, Appl	176	5	4.1	123	5	US-09-312-283B-232	Sequence 292, App
104	5	4.1	38	6	US-10-105-299-4298	Sequence 4298, Ap	177	5	4.1	131	5	US-09-540-209B-10386	Sequence 10386, A
105	5	4.1	38	6	US-10-106-698-7398	Sequence 7398, Ap	178	5	4.1	131	6	US-10-102-806-444	Sequence 444, App
106	5	4.1	41	5	US-09-710-058A-39	Sequence 39, Appl	179	5	4.1	134	5	US-09-540-209B-10438	Sequence 10438, A
107	5	4.1	41	6	US-10-043-074-28	Sequence 28, Appl	180	5	4.1	137	6	US-10-105-299-4987	Sequence 4987, Ap
108	5	4.1	42	1	PCr-US02-09785-720	Sequence 720, App	181	5	4.1	140	5	US-09-540-209B-10320	Sequence 10320, A
109	5	4.1	42	6	US-10-106-698-7413	Sequence 7413, Ap	182	5	4.1	143	6	US-10-103-313-483	Sequence 483, App
110	5	4.1	43	6	US-10-106-698-8563	Sequence 8563, Ap	183	5	4.1	144	5	US-09-573-655B-2323	Sequence 2323, Ap
111	5	4.1	44	1	PCr-US02-09785-7056	Sequence 7056, App	184	5	4.1	145	6	US-10-103-313-475	Sequence 475, App
112	5	4.1	46	6	US-10-105-299-5036	Sequence 5036, Ap	185	5	4.1	146	5	US-09-573-655B-1955	Sequence 1955, Ap
113	5	4.1	46	6	US-10-106-698-7095	Sequence 7095, Ap	186	5	4.1	146	5	US-09-990-004A-78	Sequence 78, Appl
114	5	4.1	46	6	US-10-114-666-476	Sequence 476, App	187	5	4.1	146	6	US-10-060-255-65	Sequence 65, Appl
115	5	4.1	47	1	PCr-US02-09135-165	Sequence 165, App	188	5	4.1	150	6	US-10-006-063A-196	Sequence 196, App
116	5	4.1	47	1	PCr-US02-09105-240	Sequence 240, App	189	5	4.1	150	6	US-10-006-117A-196	Sequence 196, App
117	5	4.1	47	1	PCr-US02-09257-320	Sequence 320, App	190	5	4.1	150	6	US-10-006-172A-196	Sequence 196, App
118	5	4.1	47	1	PCr-US02-09257-309	Sequence 309, App	191	5	4.1	150	6	US-10-006-172A-196	Sequence 196, App
119	5	4.1	47	1	PCr-US02-09257-309	Sequence 309, App	192	5	4.1	150	6	US-10-006-172A-196	Sequence 196, App
120	5	4.1	49	6	US-10-105-299-3193	Sequence 3193, Ap	193	5	4.1	150	6	US-10-017-527A-196	Sequence 196, App
121	5	4.1	50	1	PCr-US02-08523-10	Sequence 10, Appl	194	5	4.1	150	6	US-10-017-610A-196	Sequence 196, App
122	5	4.1	54	6	US-10-106-698-7773	Sequence 7773, Ap	195	5	4.1	150	6	US-10-006-041A-196	Sequence 196, App
123	5	4.1	58	6	US-10-106-698-4932	Sequence 4932, Ap	196	5	4.1	150	6	US-10-006-818A-196	Sequence 196, App
124	5	4.1	58	6	US-10-106-698-5579	Sequence 5579, Ap	197	5	4.1	150	6	US-10-012-121A-196	Sequence 196, App
125	5	4.1	60	1	PCr-US02-09820-17	Sequence 17, Appl	198	5	4.1	150	6	US-10-015-386A-196	Sequence 196, App
126	5	4.1	60	5	US-09-540-209B-5631	Sequence 5631, Ap	199	5	4.1	150	6	US-10-015-386A-196	Sequence 196, App
127	5	4.1	61	6	US-10-106-698-7254	Sequence 7254, Ap	200	5	4.1	150	6	US-10-119-480-110	Sequence 110, App
128	5	4.1	70	6	US-10-106-698-7295	Sequence 7295, Ap	201	5	4.1	151	6	US-10-108-605-35	Sequence 35, Appl
129	5	4.1	70	6	US-10-106-698-7933	Sequence 7933, Ap	202	5	4.1	152	1	PCr-US02-09921-621	Sequence 621, App
130	5	4.1	72	6	US-10-105-299-5492	Sequence 5492, Ap	203	5	4.1	155	6	US-10-040-895-1	Sequence 1, Appl1
131	5	4.1	73	6	US-09-573-655B-764	Sequence 764, App	204	5	4.1	155	6	US-10-121-049-380	Sequence 380, App
132	5	4.1	73	6	US-09-989-903-63	Sequence 63, Appl	205	5	4.1	155	6	US-10-121-050-380	Sequence 380, App
133	5	4.1	74	5	US-09-106-698-5468	Sequence 5468, Ap	206	5	4.1	155	6	US-10-121-053-380	Sequence 380, App
134	5	4.1	75	6	US-10-105-299-4220	Sequence 4220, Ap	207	5	4.1	155	6	US-10-121-043-380	Sequence 380, App
135	5	4.1	76	6	US-10-106-698-5038	Sequence 5038, Ap	208	5	4.1	155	6	US-10-121-044-380	Sequence 380, App
136	5	4.1	76	6	US-10-106-698-7208	Sequence 7208, Ap	209	5	4.1	155	6	US-10-121-047-380	Sequence 380, App
137	5	4.1	77	6	US-10-106-698-5716	Sequence 5716, Ap	210	5	4.1	155	6	US-10-121-054-380	Sequence 380, App
138	5	4.1	78	6	US-10-105-299-4379	Sequence 4379, Ap	211	5	4.1	155	6	US-10-121-056-380	Sequence 380, App
139	5	4.1	78	6	US-10-106-698-6440	Sequence 6440, Ap	212	5	4.1	155	6	US-10-121-057-380	Sequence 380, App
140	5	4.1	79	6	US-10-102-806-632	Sequence 632, App	213	5	4.1	155	6	US-10-121-058-380	Sequence 380, App
141	5	4.1	82	5	US-09-540-209B-6560	Sequence 6560, Ap	214	5	4.1	155	6	US-10-121-060-380	Sequence 380, App
142	5	4.1	82	6	US-10-107-431-189	Sequence 189, App	215	5	4.1	155	6	US-10-121-063-380	Sequence 380, App
143	5	4.1	84	6	US-10-106-698-7308	Sequence 7308, Ap	216	5	4.1	155	6	US-10-123-108-380	Sequence 380, App
144	5	4.1	85	5	US-09-540-209B-8218	Sequence 8218, Ap	217	5	4.1	155	6	US-10-123-109-380	Sequence 380, App
145	5	4.1	85	5	US-09-540-209B-10257	Sequence 10257, A	218	5	4.1	155	6	US-10-123-156-380	Sequence 380, App
146	5	4.1	85	6	US-10-060-255-52	Sequence 52, Appl	219	5	4.1	155	6	US-10-123-157-380	Sequence 380, App
147	5	4.1	85	6	US-10-119-480-112	Sequence 112, App	220	5	4.1	155	6	US-10-123-212-380	Sequence 380, App
148	5	4.1	86	5	US-09-573-655B-2446	Sequence 2446, Ap	221	5	4.1	155	6	US-10-123-213-380	Sequence 380, App
149	5	4.1	86	5	US-09-990-004A-71	Sequence 71, Appl	222	5	4.1	155	6	US-10-123-109-380	Sequence 380, App
150	5	4.1	88	6	US-10-106-698-4335	Sequence 4335, Ap	223	5	4.1	155	6	US-10-121-041-380	Sequence 380, App
151	5	4.1	95	5	US-09-540-209B-8687	Sequence 8687, Ap	224	5	4.1	155	6	US-10-121-045-380	Sequence 380, App
152	5	4.1	102	5	US-09-540-209B-8744	Sequence 8744, Ap	225	5	4.1	155	6	US-10-121-046-380	Sequence 380, App
153	5	4.1	102	6	US-10-106-698-4988	Sequence 4988, Ap	226	5	4.1	155	6	US-10-121-051-380	Sequence 380, App
154	5	4.1	103	5	US-09-573-655B-1457	Sequence 1457, Ap	227	5	4.1	157	7	US-60-365-384-625	Sequence 625, App
155	5	4.1	106	7	US-60-365-384-608	Sequence 608, App	228	5	4.1	159	6	US-10-106-698-4748	Sequence 4748, Ap
156	5	4.1	107	6	PCr-US02-09921-1143	Sequence 344, App	229	5	4.1	162	5	US-09-573-655B-2460	Sequence 2460, Ap
157	5	4.1	109	1	US-10-116-355-344	Sequence 1143, Ap	230	5	4.1	162	5	US-09-540-209B-7657	Sequence 7657, Ap
158	5	4.1	115	5	US-09-540-209B-5268	Sequence 5268, Ap	231	5	4.1	163	6	US-10-017-066-7	Sequence 7, Appl1
159	5	4.1	115	5	US-09-990-004A-74	Sequence 74, Appl	232	5	4.1	164	5	US-09-312-283B-385	Sequence 385, App
160	5	4.1	115	6	US-10-060-255-76	Sequence 76, Appl	233	5	4.1	164	6	US-10-103-196-21	Sequence 21, Appl
161	5	4.1	119	5	US-09-990-004A-70	Sequence 70, Appl	234	5	4.1	165	1	PCr-US02-10824-115	Sequence 115, App
162	5	4.1	121	6	US-10-006-063A-354	Sequence 354, App	235	5	4.1	169	1	PCr-US02-09785-862	Sequence 862, App
163	5	4.1	121	6	US-10-006-117A-354	Sequence 354, App	236	5	4.1	172	5	US-09-540-209B-7055	Sequence 7055, Ap
164	5	4.1	121	6	US-10-006-130A-354	Sequence 354, App	237	5	4.1	172	6	US-10-115-192-6	Sequence 6, Appl1
165	5	4.1	121	6	US-10-006-172A-354	Sequence 354, App	238	5	4.1	176	6	US-10-102-806-657	Sequence 657, App
166	5	4.1	121	6	US-10-006-768A-354	Sequence 354, App	239	5	4.1	176	6	US-10-119-480-218	Sequence 218, App
167	5	4.1	121	6	US-10-106-698-6760	Sequence 6760, Ap	240	5	4.1	176	6	US-10-121-049-98	Sequence 98, Appl
168	5	4.1	121	6	US-10-017-527A-354	Sequence 354, App	241	5	4.1	176	6	US-10-121-050-98	Sequence 98, Appl
169	5	4.1	121	6	US-10-017-610A-354	Sequence 354, App	242	5	4.1	176	6	US-10-121-053-98	Sequence 98, Appl
170	5	4.1	121	6	US-10-006-041A-354	Sequence 354, App	243	5	4.1	176	6	US-10-121-043-98	Sequence 98, Appl
171	5	4.1	121	6	US-10-006-818A-354	Sequence 354, App	244	5	4.1	176	6	US-10-121-044-98	Sequence 98, Appl
172	5	4.1	121	6	US-10-012-121A-354	Sequence 354, App	245	5	4.1	176	6	US-10-121-047-98	Sequence 98, Appl

246	5	4.1	176	6	US-10-121-054-98	Sequence 98, Appl	319	5	4.1	249	6	US-10-121-058-110	Sequence 110, App
247	5	4.1	176	6	US-10-121-056-98	Sequence 98, Appl	320	5	4.1	249	6	US-10-121-060-110	Sequence 110, App
248	5	4.1	176	6	US-10-121-057-98	Sequence 98, Appl	321	5	4.1	249	6	US-10-121-063-110	Sequence 110, App
249	5	4.1	176	6	US-10-121-058-98	Sequence 98, Appl	322	5	4.1	249	6	US-10-112-267-56	Sequence 56, Appl
250	5	4.1	176	6	US-10-121-060-98	Sequence 98, Appl	323	5	4.1	249	6	US-10-123-108-110	Sequence 110, App
251	5	4.1	176	6	US-10-121-063-98	Sequence 98, Appl	324	5	4.1	249	6	US-10-123-154-110	Sequence 110, App
252	5	4.1	176	6	US-10-123-108-98	Sequence 98, Appl	325	5	4.1	249	6	US-10-123-156-110	Sequence 110, App
253	5	4.1	176	6	US-10-123-154-98	Sequence 98, Appl	326	5	4.1	249	6	US-10-123-157-110	Sequence 110, App
254	5	4.1	176	6	US-10-123-156-98	Sequence 98, Appl	327	5	4.1	249	6	US-10-123-212-110	Sequence 110, App
255	5	4.1	176	6	US-10-123-157-98	Sequence 98, Appl	328	5	4.1	249	6	US-10-123-213-110	Sequence 110, App
256	5	4.1	176	6	US-10-123-212-98	Sequence 98, Appl	329	5	4.1	249	6	US-10-123-109-110	Sequence 110, App
257	5	4.1	176	6	US-10-123-213-98	Sequence 98, Appl	330	5	4.1	249	6	US-10-121-041-110	Sequence 110, App
258	5	4.1	176	6	US-10-123-109-98	Sequence 98, Appl	331	5	4.1	249	6	US-10-121-045-110	Sequence 110, App
259	5	4.1	176	6	US-10-121-041-98	Sequence 98, Appl	332	5	4.1	249	6	US-10-121-046-110	Sequence 110, App
260	5	4.1	176	6	US-10-121-045-98	Sequence 98, Appl	333	5	4.1	249	6	US-10-121-051-110	Sequence 110, App
261	5	4.1	176	6	US-10-121-046-98	Sequence 98, Appl	334	5	4.1	250	6	US-10-121-049-320	Sequence 320, App
262	5	4.1	176	6	US-10-121-051-98	Sequence 98, Appl	335	5	4.1	250	6	US-10-121-050-320	Sequence 320, App
263	5	4.1	179	5	US-09-540-209B-7366	Sequence 7366, Ap	336	5	4.1	250	6	US-10-121-053-320	Sequence 320, App
264	5	4.1	183	6	US-10-106-698-4841	Sequence 4841, Ap	337	5	4.1	250	6	US-10-121-043-320	Sequence 320, App
265	5	4.1	193	5	US-09-573-655B-2345	Sequence 2345, Ap	338	5	4.1	250	6	US-10-121-044-320	Sequence 320, App
266	5	4.1	193	6	US-10-102-806-713	Sequence 713, App	339	5	4.1	250	6	US-10-121-047-320	Sequence 320, App
267	5	4.1	196	5	US-09-990-004A-73	Sequence 73, Appl	340	5	4.1	250	6	US-10-121-054-320	Sequence 320, App
268	5	4.1	198	6	US-10-060-255-79	Sequence 79, Appl	341	5	4.1	250	6	US-10-121-056-320	Sequence 320, App
269	5	4.1	199	5	US-09-540-209B-7450	Sequence 7450, Ap	342	5	4.1	250	6	US-10-121-057-320	Sequence 320, App
270	5	4.1	200	6	US-10-105-931-11	Sequence 11, Appl	343	5	4.1	250	6	US-10-121-058-320	Sequence 320, App
271	5	4.1	202	5	US-09-540-209B-6069	Sequence 6069, Ap	344	5	4.1	250	6	US-10-121-060-320	Sequence 320, App
272	5	4.1	202	5	US-09-540-209B-8896	Sequence 8896, Ap	345	5	4.1	250	6	US-10-121-063-320	Sequence 320, App
273	5	4.1	204	6	US-10-023-171-29	Sequence 29, Appl	346	5	4.1	250	6	US-10-112-267-16	Sequence 16, Appl
274	5	4.1	205	5	US-09-540-209B-7817	Sequence 7817, Ap	347	5	4.1	250	6	US-10-123-108-320	Sequence 320, App
275	5	4.1	206	1	PCT-US02-09921-864	Sequence 864, App	348	5	4.1	250	6	US-10-123-154-320	Sequence 320, App
276	5	4.1	207	1	PCT-US02-09921-658	Sequence 658, App	349	5	4.1	250	6	US-10-123-156-320	Sequence 320, App
277	5	4.1	209	5	US-09-540-209B-5497	Sequence 5497, Ap	350	5	4.1	250	6	US-10-123-157-320	Sequence 320, App
278	5	4.1	211	5	US-09-540-209B-7149	Sequence 7149, Ap	351	5	4.1	250	6	US-10-123-212-320	Sequence 320, App
279	5	4.1	211	5	US-09-540-209B-7708	Sequence 7708, Ap	352	5	4.1	250	6	US-10-123-213-320	Sequence 320, App
280	5	4.1	216	1	PCT-US02-09785-1015	Sequence 1015, Ap	353	5	4.1	250	6	US-10-123-109-320	Sequence 320, App
281	5	4.1	217	6	US-10-105-299-5152	Sequence 5152, Ap	354	5	4.1	250	6	US-10-121-041-320	Sequence 320, App
282	5	4.1	218	6	US-10-105-299-5797	Sequence 5797, Ap	355	5	4.1	250	6	US-10-121-045-320	Sequence 320, App
283	5	4.1	223	5	US-09-895-913A-84	Sequence 84, Appl	356	5	4.1	250	6	US-10-121-046-320	Sequence 320, App
284	5	4.1	224	1	PCT-US02-09921-1101	Sequence 1101, Ap	357	5	4.1	250	6	US-10-121-051-320	Sequence 320, App
285	5	4.1	225	5	US-09-540-209B-6866	Sequence 6866, Ap	358	5	4.1	251	5	US-09-540-209B-8488	Sequence 8488, Ap
286	5	4.1	226	6	US-10-106-698-6008	Sequence 6008, Ap	359	5	4.1	251	5	US-09-981-566A-51	Sequence 51, Appl
287	5	4.1	227	6	US-10-103-313-468	Sequence 468, App	360	5	4.1	253	6	US-10-102-627-66	Sequence 66, Appl
288	5	4.1	229	5	US-09-540-209B-9700	Sequence 9700, Ap	361	5	4.1	255	6	US-10-114-666-454	Sequence 454, App
289	5	4.1	231	6	US-10-106-698-4582	Sequence 4582, Ap	362	5	4.1	255	7	US-60-370-796-13	Sequence 13, Appl
290	5	4.1	232	6	US-10-106-698-5299	Sequence 5299, Ap	363	5	4.1	257	5	US-09-813-453A-13	Sequence 13, Appl
291	5	4.1	237	1	PCT-US02-09921-773	Sequence 773, App	364	5	4.1	260	5	US-09-989-903-2	Sequence 2, Appl
292	5	4.1	237	5	US-09-540-209B-7829	Sequence 7829, Ap	365	5	4.1	261	5	US-09-540-209B-5752	Sequence 5752, Ap
293	5	4.1	239	5	US-09-540-209B-7225	Sequence 7225, Ap	366	5	4.1	261	6	US-10-006-063A-402	Sequence 402, App
294	5	4.1	239	5	US-09-990-004A-65	Sequence 65, Appl	367	5	4.1	261	6	US-10-006-117A-402	Sequence 402, App
295	5	4.1	240	5	US-09-573-655B-937	Sequence 937, App	368	5	4.1	261	6	US-10-006-130A-402	Sequence 402, App
296	5	4.1	240	5	US-09-540-209B-6433	Sequence 6433, Ap	369	5	4.1	261	6	US-10-006-172A-402	Sequence 402, App
297	5	4.1	241	6	US-10-112-267-64	Sequence 64, Appl	370	5	4.1	261	6	US-10-006-768A-402	Sequence 402, App
298	5	4.1	242	6	US-10-112-267-63	Sequence 63, Appl	371	5	4.1	261	6	US-10-017-527A-402	Sequence 402, App
299	5	4.1	243	6	US-10-112-267-62	Sequence 62, Appl	372	5	4.1	261	6	US-10-017-610A-402	Sequence 402, App
300	5	4.1	244	6	US-10-112-267-61	Sequence 61, Appl	373	5	4.1	261	6	US-10-006-041A-402	Sequence 402, App
301	5	4.1	245	6	US-10-112-267-60	Sequence 60, Appl	374	5	4.1	261	6	US-10-006-081A-402	Sequence 402, App
302	5	4.1	246	5	US-09-573-655B-23	Sequence 23, Appl	375	5	4.1	261	6	US-10-012-121A-402	Sequence 402, App
303	5	4.1	246	6	US-10-112-267-59	Sequence 59, Appl	376	5	4.1	261	6	US-10-015-386A-402	Sequence 402, App
304	5	4.1	247	6	US-10-112-267-58	Sequence 58, Appl	377	5	4.1	261	6	US-10-015-387A-402	Sequence 402, App
305	5	4.1	247	6	US-10-120-414-79	Sequence 79, Appl	378	5	4.1	261	6	US-10-121-049-546	Sequence 546, App
306	5	4.1	248	6	US-10-103-196-15	Sequence 15, Appl	379	5	4.1	261	6	US-10-121-050-546	Sequence 546, App
307	5	4.1	248	6	US-10-112-267-57	Sequence 57, Appl	380	5	4.1	261	6	US-10-121-053-546	Sequence 546, App
308	5	4.1	249	1	PCT-US02-10421-2897	Sequence 2897, Ap	381	5	4.1	261	6	US-10-121-043-546	Sequence 546, App
309	5	4.1	249	6	US-10-112-699-2897	Sequence 2897, Ap	382	5	4.1	261	6	US-10-121-044-546	Sequence 546, App
310	5	4.1	249	6	US-10-121-049-110	Sequence 110, App	383	5	4.1	261	6	US-10-121-047-546	Sequence 546, App
311	5	4.1	249	6	US-10-121-050-110	Sequence 110, App	384	5	4.1	261	6	US-10-121-054-546	Sequence 546, App
312	5	4.1	249	6	US-10-121-053-110	Sequence 110, App	385	5	4.1	261	6	US-10-121-056-546	Sequence 546, App
313	5	4.1	249	6	US-10-121-043-110	Sequence 110, App	386	5	4.1	261	6	US-10-121-057-546	Sequence 546, App
314	5	4.1	249	6	US-10-121-044-110	Sequence 110, App	387	5	4.1	261	6	US-10-121-058-546	Sequence 546, App
315	5	4.1	249	6	US-10-121-047-110	Sequence 110, App	388	5	4.1	261	6	US-10-121-060-546	Sequence 546, App
316	5	4.1	249	6	US-10-121-054-110	Sequence 110, App	389	5	4.1	261	6	US-10-121-063-546	Sequence 546, App
317	5	4.1	249	6	US-10-121-056-110	Sequence 110, App	390	5	4.1	261	6	US-10-123-108-546	Sequence 546, App
318	5	4.1	249	6	US-10-121-057-110	Sequence 110, App	391	5	4.1	261	6	US-10-123-134-546	Sequence 546, App

392	5	4.1	261	6	US-10-123-156-546	Sequence 546, App	465	5	4.1	305	5	US-09-540-209B-10050	Sequence 10050, A
393	5	4.1	261	6	US-10-123-157-546	Sequence 546, App	466	5	4.1	305	5	US-09-990-004A-188	Sequence 188, App
394	5	4.1	261	6	US-10-123-212-546	Sequence 546, App	467	5	4.1	305	6	US-10-106-698-4414	Sequence 4414, Ap
395	5	4.1	261	6	US-10-123-213-546	Sequence 546, App	468	5	4.1	307	5	US-09-743-207-12	Sequence 12, Appl
396	5	4.1	261	6	US-10-123-109-546	Sequence 546, App	469	5	4.1	308	5	US-09-981-566A-75	Sequence 75, Appl
397	5	4.1	261	6	US-10-121-041-546	Sequence 546, App	470	5	4.1	310	5	US-09-540-209B-5549	Sequence 5549, Ap
398	5	4.1	261	6	US-10-121-045-546	Sequence 546, App	471	5	4.1	311	5	US-09-907-218-55	Sequence 55, Appl
399	5	4.1	261	6	US-10-121-046-546	Sequence 546, App	472	5	4.1	311	6	US-10-106-698-5688	Sequence 5688, Ap
400	5	4.1	261	6	US-10-121-051-546	Sequence 546, App	473	5	4.1	312	7	US-60-372-508-12	Sequence 12, Appl
401	5	4.1	262	6	US-10-114-666-457	Sequence 457, App	474	5	4.1	313	1	PCT-US02-03635-40	Sequence 40, Appl
402	5	4.1	263	5	US-09-540-209B-6940	Sequence 6940, App	475	5	4.1	313	6	US-10-121-746-81	Sequence 81, Appl
403	5	4.1	265	5	US-09-540-209B-5433	Sequence 5433, Ap	476	5	4.1	314	6	US-10-032-106-10	Sequence 10, Appl
404	5	4.1	265	5	US-09-540-209B-6712	Sequence 6712, Ap	477	5	4.1	315	1	PCT-US02-09923-10	Sequence 10, Appl
405	5	4.1	266	1	PCT-US02-09921-804	Sequence 804, Appl	478	5	4.1	315	5	US-09-965-422-20	Sequence 20, Appl
406	5	4.1	266	6	US-10-089-700-3	Sequence 3, Appli	479	5	4.1	315	5	US-09-965-422-22	Sequence 22, Appl
407	5	4.1	269	6	US-10-103-313-319	Sequence 319, App	480	5	4.1	315	5	US-09-965-422-24	Sequence 24, Appl
408	5	4.1	272	5	US-09-540-209B-6270	Sequence 6270, Ap	481	5	4.1	316	1	PCT-US02-01339-12	Sequence 12, Appl
409	5	4.1	273	6	US-10-106-698-4937	Sequence 4937, Ap	482	5	4.1	316	5	US-09-978-403A-137	Sequence 137, App
410	5	4.1	273	6	US-10-121-049-540	Sequence 540, App	483	5	4.1	316	5	US-09-978-544A-137	Sequence 137, App
411	5	4.1	273	6	US-10-121-050-540	Sequence 540, App	484	5	4.1	316	5	US-09-978-681A-137	Sequence 137, App
412	5	4.1	273	6	US-10-121-053-540	Sequence 540, App	485	5	4.1	316	5	US-09-978-757A-137	Sequence 137, App
413	5	4.1	273	6	US-10-121-043-540	Sequence 540, App	486	5	4.1	316	5	US-09-978-757A-137	Sequence 137, App
414	5	4.1	273	6	US-10-121-044-540	Sequence 540, App	487	5	4.1	316	5	US-09-999-831A-137	Sequence 137, App
415	5	4.1	273	6	US-10-121-047-540	Sequence 540, App	488	5	4.1	316	5	US-09-999-829A-137	Sequence 137, App
416	5	4.1	273	6	US-10-121-054-540	Sequence 540, App	489	5	4.1	316	5	US-09-540-209B-6651	Sequence 6651, Ap
417	5	4.1	273	6	US-10-121-056-540	Sequence 540, App	490	5	4.1	316	5	US-09-990-004A-62	Sequence 62, Appl
418	5	4.1	273	6	US-10-121-057-540	Sequence 540, App	491	5	4.1	316	6	US-10-013-921A-137	Sequence 137, App
419	5	4.1	273	6	US-10-121-058-540	Sequence 540, App	492	5	4.1	316	6	US-10-013-929A-137	Sequence 137, App
420	5	4.1	273	6	US-10-121-060-540	Sequence 540, App	493	5	4.1	316	6	US-10-013-918A-137	Sequence 137, App
421	5	4.1	273	6	US-10-121-063-540	Sequence 540, App	494	5	4.1	316	6	US-10-017-082A-137	Sequence 137, App
422	5	4.1	273	6	US-10-123-108-540	Sequence 540, App	495	5	4.1	317	1	PCT-US02-09921-707	Sequence 707, App
423	5	4.1	273	6	US-10-123-154-540	Sequence 540, App	496	5	4.1	317	5	US-09-540-209B-7157	Sequence 7157, Ap
424	5	4.1	273	6	US-10-123-156-540	Sequence 540, App	497	5	4.1	322	7	US-60-365-384-314	Sequence 314, App
425	5	4.1	273	6	US-10-123-157-540	Sequence 540, App	498	5	4.1	323	5	US-09-540-209B-8468	Sequence 8468, Ap
426	5	4.1	273	6	US-10-123-212-540	Sequence 540, App	499	5	4.1	324	1	PCT-US02-09923-25	Sequence 25, Appl
427	5	4.1	273	6	US-10-123-213-540	Sequence 540, App	500	5	4.1	324	5	US-09-573-655B-2119	Sequence 2119, Ap
428	5	4.1	273	6	US-10-123-109-540	Sequence 540, App	501	5	4.1	326	6	US-10-108-605-19	Sequence 19, Appl
429	5	4.1	273	6	US-10-121-041-540	Sequence 540, App	502	5	4.1	327	1	PCT-US02-03635-39	Sequence 39, Appl
430	5	4.1	273	6	US-10-121-045-540	Sequence 540, App	503	5	4.1	327	6	US-10-125-459-8	Sequence 8, Appli
431	5	4.1	273	6	US-10-121-046-540	Sequence 540, App	504	5	4.1	328	1	PCT-US02-08288-2	Sequence 2, Appli
432	5	4.1	273	6	US-10-121-051-540	Sequence 540, App	505	5	4.1	328	6	US-10-106-698-4635	Sequence 4635, Ap
433	5	4.1	274	1	PCT-US02-09921-978	Sequence 978, App	506	5	4.1	332	5	US-09-540-209B-8282	Sequence 8282, Ap
434	5	4.1	274	6	US-09-540-209B-8195	Sequence 8195, Ap	507	5	4.1	332	6	US-10-106-698-6370	Sequence 6370, Ap
435	5	4.1	274	6	US-10-121-988-74	Sequence 74, Appl	508	5	4.1	333	5	US-09-573-655B-1256	Sequence 1256, Ap
436	5	4.1	279	5	US-09-573-655B-978	Sequence 978, App	509	5	4.1	334	5	US-09-540-209B-9829	Sequence 9829, Ap
437	5	4.1	279	5	US-09-540-209B-7582	Sequence 7582, Ap	510	5	4.1	335	5	US-09-540-209B-7085	Sequence 7085, Ap
438	5	4.1	280	6	US-10-115-899-5	Sequence 5, Appli	511	5	4.1	338	5	US-09-312-283B-325	Sequence 325, App
439	5	4.1	280	6	US-10-115-899-8	Sequence 8, Appli	512	5	4.1	338	5	US-09-540-209B-7491	Sequence 7491, Ap
440	5	4.1	281	5	US-09-540-209B-6267	Sequence 6267, Ap	513	5	4.1	341	5	US-09-540-209B-7542	Sequence 7542, Ap
441	5	4.1	282	1	PCT-US02-09785-815	Sequence 815, App	514	5	4.1	344	5	US-09-540-209B-8052	Sequence 8052, Ap
442	5	4.1	283	5	US-09-540-209B-10359	Sequence 10359, A	515	5	4.1	345	1	PCT-US02-09944-478	Sequence 478, App
443	5	4.1	284	5	US-09-540-209B-7292	Sequence 7292, Ap	516	5	4.1	345	6	US-10-106-698-6316	Sequence 6316, Ap
444	5	4.1	287	5	US-09-762-154-18	Sequence 18, Appl	517	5	4.1	346	1	PCT-US02-07999-82	Sequence 82, Appl
445	5	4.1	288	5	US-09-540-209B-7740	Sequence 7740, Ap	518	5	4.1	346	1	PCT-US01-09366A-2	Sequence 2, Appli
446	5	4.1	289	6	US-10-011-585A-167	Sequence 167, App	519	5	4.1	346	1	US-09-540-209B-5775	Sequence 5775, Ap
447	5	4.1	290	1	PCT-US02-10303-23	Sequence 23, Appl	520	5	4.1	347	5	US-09-602-777A-436	Sequence 436, App
448	5	4.1	290	1	PCT-US02-10371-23	Sequence 23, Appl	521	5	4.1	348	5	US-09-540-209B-9575	Sequence 9575, Ap
449	5	4.1	290	5	US-09-540-209B-7640	Sequence 7640, Ap	522	5	4.1	350	5	US-09-602-777A-290	Sequence 290, App
450	5	4.1	290	6	US-10-102-806-494	Sequence 494, App	523	5	4.1	351	5	US-09-573-655B-1835	Sequence 1835, Ap
451	5	4.1	290	6	US-10-115-609-23	Sequence 23, Appl	524	5	4.1	351	6	US-10-106-698-4697	Sequence 4697, Ap
452	5	4.1	290	6	US-10-115-615-23	Sequence 23, Appl	525	5	4.1	355	5	US-09-540-209B-6354	Sequence 6354, App
453	5	4.1	293	5	US-09-635-554-2	Sequence 2, Appli	526	5	4.1	356	5	US-09-573-655B-303	Sequence 303, App
454	5	4.1	293	6	US-10-084-971-2	Sequence 10, Appl	527	5	4.1	357	7	US-60-365-264-651	Sequence 651, App
455	5	4.1	293	7	US-60-372-508-10	Sequence 6860, Ap	528	5	4.1	358	6	US-10-104-340-2	Sequence 2, Appli
456	5	4.1	294	5	US-09-540-209B-6860	Sequence 219, App	529	5	4.1	358	6	US-10-106-698-6181	Sequence 6181, Ap
457	5	4.1	295	5	US-09-573-655B-219	Sequence 219, App	530	5	4.1	359	5	US-09-540-209B-5642	Sequence 5642, Ap
458	5	4.1	299	5	US-09-540-209B-5571	Sequence 5571, Ap	531	5	4.1	361	1	PCT-US02-09944-570	Sequence 570, App
459	5	4.1	300	5	US-09-573-655B-394	Sequence 394, App	532	5	4.1	361	6	US-10-108-605-255	Sequence 255, App
460	5	4.1	300	5	US-09-573-655B-1582	Sequence 1582, Ap	533	5	4.1	361	6	US-10-106-698-5093	Sequence 5093, Ap
461	5	4.1	302	5	US-09-573-655B-1003	Sequence 1003, Ap	534	5	4.1	363	1	PCT-US02-09944-412	Sequence 412, App
462	5	4.1	303	5	US-09-540-209B-7767	Sequence 7767, Ap	535	5	4.1	363	5	US-09-540-209B-7020	Sequence 7020, Ap
463	5	4.1	303	5	US-09-540-209B-8459	Sequence 8459, Ap	536	5	4.1	363	6	US-10-006-063A-72	Sequence 72, Appl
464	5	4.1	304	5	US-09-573-655B-102	Sequence 102, App	537	5	4.1				

538	5	4.1	363	6	US-10-006-117A-72	Sequence 72, Appl	611	5	4.1	435	5	US-09-540-209B-7964	Sequence 7964, Ap
539	5	4.1	363	6	US-10-006-130A-72	Sequence 72, Appl	612	5	4.1	437	5	US-09-540-209B-7669	Sequence 7669, Ap
540	5	4.1	363	6	US-10-006-172A-72	Sequence 72, Appl	613	5	4.1	437	5	US-09-540-209B-9492	Sequence 9492, Ap
541	5	4.1	363	6	US-10-006-768A-72	Sequence 72, Appl	614	5	4.1	438	1	PCT-US01-25881-21	Sequence 21, Appl
542	5	4.1	363	6	US-10-017-527A-72	Sequence 72, Appl	615	5	4.1	439	5	US-09-540-209B-6330	Sequence 6330, Ap
543	5	4.1	363	6	US-10-017-610A-72	Sequence 72, Appl	616	5	4.1	440	5	US-09-743-207-2	Sequence 2, Appl
544	5	4.1	363	6	US-10-006-041A-72	Sequence 72, Appl	617	5	4.1	440	5	US-09-540-209B-6875	Sequence 6875, Ap
545	5	4.1	363	6	US-10-006-018A-72	Sequence 72, Appl	618	5	4.1	444	4	US-08-945-821D-4	Sequence 4, Appl
546	5	4.1	363	6	US-10-012-121A-72	Sequence 72, Appl	619	5	4.1	444	4	US-08-945-821D-6	Sequence 6, Appl
547	5	4.1	363	6	US-10-015-386A-72	Sequence 72, Appl	620	5	4.1	444	5	US-09-573-655B-1255	Sequence 1255, Ap
548	5	4.1	363	6	US-10-015-387A-72	Sequence 72, Appl	621	5	4.1	444	6	US-10-023-839-3	Sequence 3, Appl
549	5	4.1	364	7	US-60-365-264-680	Sequence 680, App	622	5	4.1	444	6	US-10-023-839-5	Sequence 5, Appl
550	5	4.1	372	7	US-60-366-832-14	Sequence 14, Appl	623	5	4.1	446	6	US-09-573-655B-120	Sequence 120, App
551	5	4.1	374	5	US-09-540-209B-8992	Sequence 8992, Ap	624	5	4.1	446	6	US-10-103-313-326	Sequence 326, App
552	5	4.1	381	5	US-09-540-209B-6324	Sequence 6324, Ap	625	5	4.1	448	1	PCT-US02-09944-751	Sequence 751, App
553	5	4.1	381	5	US-09-540-209B-7389	Sequence 7389, Ap	626	5	4.1	449	5	US-09-540-209B-5270	Sequence 5270, Ap
554	5	4.1	383	6	US-10-108-605-105	Sequence 105, App	627	5	4.1	450	1	PCT-US02-08523-13	Sequence 13, Appl
555	5	4.1	387	6	US-10-106-698-6168	Sequence 6168, Ap	628	5	4.1	450	7	US-60-366-892-15	Sequence 15, Appl
556	5	4.1	387	7	US-60-365-384-539	Sequence 539, App	629	5	4.1	452	5	US-09-540-209B-5473	Sequence 5473, Ap
557	5	4.1	389	5	US-09-573-655B-689	Sequence 689, App	630	5	4.1	452	5	US-09-540-209B-6551	Sequence 6551, Ap
558	5	4.1	389	5	US-09-573-655B-1042	Sequence 1042, Ap	631	5	4.1	453	5	US-09-978-403A-69	Sequence 69, Appl
559	5	4.1	389	5	US-09-573-655B-1762	Sequence 1762, Ap	632	5	4.1	453	5	US-09-978-344A-69	Sequence 69, Appl
560	5	4.1	392	5	US-09-540-209B-6376	Sequence 6376, Ap	633	5	4.1	453	5	US-09-978-681A-69	Sequence 69, Appl
561	5	4.1	392	6	US-10-117-532-10	Sequence 10, Appl	634	5	4.1	453	5	US-09-978-757A-69	Sequence 69, Appl
562	5	4.1	394	6	US-10-117-532-5	Sequence 5, Appl	635	5	4.1	453	5	US-09-978-564A-69	Sequence 69, Appl
563	5	4.1	395	5	US-09-573-655B-1317	Sequence 1317, Ap	636	5	4.1	453	5	US-09-999-831A-69	Sequence 69, Appl
564	5	4.1	396	1	PCT-US02-09921-1113	Sequence 1113, Ap	637	5	4.1	453	5	US-09-999-829A-69	Sequence 69, Appl
565	5	4.1	397	5	US-09-006-428A-2	Sequence 2, Appl	638	5	4.1	453	6	US-10-013-921A-69	Sequence 69, Appl
566	5	4.1	397	5	US-09-006-428A-19	Sequence 19, Appl	639	5	4.1	453	6	US-10-013-929A-69	Sequence 69, Appl
567	5	4.1	399	5	US-09-763-154-90	Sequence 90, App	640	5	4.1	453	6	US-10-013-918A-69	Sequence 69, Appl
568	5	4.1	400	5	US-09-540-209B-5896	Sequence 5896, Ap	641	5	4.1	453	6	US-10-017-082A-69	Sequence 69, Appl
569	5	4.1	401	5	US-09-901-556A-3	Sequence 3, Appl	642	5	4.1	453	6	US-10-106-698-5604	Sequence 5604, Ap
570	5	4.1	402	5	US-09-540-209B-9410	Sequence 9410, Ap	643	5	4.1	455	1	PCT-US01-25881-4	Sequence 4, Appl
571	5	4.1	403	1	PCT-US02-07826-149	Sequence 149, App	644	5	4.1	456	6	US-10-107-431-87	Sequence 87, Appl
572	5	4.1	403	6	US-09-573-655B-1452	Sequence 1452, Ap	645	5	4.1	458	1	PCT-US01-25881-3	Sequence 3, Appl
573	5	4.1	403	6	US-10-097-340-149	Sequence 149, App	646	5	4.1	458	1	PCT-US01-25881-27	Sequence 27, Appl
574	5	4.1	404	5	US-09-540-209B-7980	Sequence 7980, Ap	647	5	4.1	458	6	US-10-115-415-4	Sequence 4, Appl
575	5	4.1	405	5	US-09-540-209B-9615	Sequence 9615, Ap	648	5	4.1	458	6	US-10-115-671-4	Sequence 4, Appl
576	5	4.1	405	6	US-10-109-550-2	Sequence 2, Appl	649	5	4.1	458	6	US-10-115-688-4	Sequence 4, Appl
577	5	4.1	406	6	US-10-117-532-4	Sequence 4, Appl	650	5	4.1	458	6	US-10-115-685-4	Sequence 4, Appl
578	5	4.1	407	6	US-10-117-532-2	Sequence 2, Appl	651	5	4.1	458	6	US-10-116-260-4	Sequence 4, Appl
579	5	4.1	408	5	US-09-749-728B-69	Sequence 69, Appl	652	5	4.1	458	6	US-10-116-561-4	Sequence 4, Appl
580	5	4.1	408	5	US-09-573-655B-210	Sequence 210, App	653	5	4.1	461	5	US-09-978-917A-2	Sequence 2, Appl
581	5	4.1	409	1	PCT-US01-25881-20	Sequence 20, Appl	654	5	4.1	461	5	US-09-997-623-2	Sequence 2, Appl
582	5	4.1	411	5	US-09-749-728B-1	Sequence 1, Appl	655	5	4.1	467	1	PCT-US02-09921-688	Sequence 688, App
583	5	4.1	411	5	US-09-895-913A-292	Sequence 292, App	656	5	4.1	467	5	US-09-540-209B-7672	Sequence 7672, Ap
584	5	4.1	412	5	US-09-573-655B-711	Sequence 711, App	657	5	4.1	469	1	PCT-US02-07826-171	Sequence 171, App
585	5	4.1	412	5	US-09-573-655B-1217	Sequence 1217, Ap	658	5	4.1	469	1	PCT-US02-07826-173	Sequence 173, App
586	5	4.1	415	6	US-10-102-806-437	Sequence 437, App	659	5	4.1	469	6	US-09-573-655B-1089	Sequence 1089, Ap
587	5	4.1	416	5	US-09-006-428A-1	Sequence 1, Appl	660	5	4.1	469	6	US-10-097-340-171	Sequence 171, App
588	5	4.1	416	5	US-09-006-428A-17	Sequence 17, Appl	661	5	4.1	469	6	US-10-097-340-173	Sequence 173, App
589	5	4.1	419	5	US-09-978-917A-4	Sequence 4, Appl	662	5	4.1	471	6	US-10-100-679-96	Sequence 96, Appl
590	5	4.1	419	5	US-09-997-623-4	Sequence 4, Appl	663	5	4.1	476	7	US-60-363-384-574	Sequence 574, App
591	5	4.1	419	5	US-09-540-209B-6424	Sequence 6424, Ap	664	5	4.1	481	5	US-09-540-209B-6068	Sequence 6068, Ap
592	5	4.1	419	5	US-09-540-209B-7719	Sequence 7719, Ap	665	5	4.1	482	6	US-10-106-698-4627	Sequence 4627, Ap
593	5	4.1	420	5	US-09-573-655B-1611	Sequence 1611, Ap	666	5	4.1	484	5	US-09-573-655B-1025	Sequence 1025, Ap
594	5	4.1	420	5	US-09-573-655B-2264	Sequence 2264, Ap	667	5	4.1	484	5	US-09-573-655B-1580	Sequence 1580, Ap
595	5	4.1	420	5	US-09-540-209B-8311	Sequence 8311, Ap	668	5	4.1	488	6	US-10-109-310-15	Sequence 15, Appl
596	5	4.1	422	5	US-09-540-209B-5265	Sequence 5265, Ap	669	5	4.1	489	1	PCT-US02-10818-15	Sequence 15, Appl
597	5	4.1	423	6	US-10-100-679-95	Sequence 95, Appl	670	5	4.1	489	5	US-09-991-150-138	Sequence 138, App
598	5	4.1	423	6	US-10-107-431-31	Sequence 31, Appl	671	5	4.1	490	6	US-10-105-931-26	Sequence 26, Appl
599	5	4.1	424	1	PCT-US02-09944-705	Sequence 705, App	672	5	4.1	491	5	US-09-863-776-34	Sequence 34, Appl
600	5	4.1	424	5	US-09-573-655B-1484	Sequence 1484, Ap	673	5	4.1	495	5	US-09-915-181A-7	Sequence 7, Appl
601	5	4.1	426	6	US-10-113-113-2	Sequence 2, Appl	674	5	4.1	496	1	PCT-US02-09944-440	Sequence 440, App
602	5	4.1	426	5	US-09-540-209B-5807	Sequence 5807, Ap	675	5	4.1	496	6	US-10-067-741-46	Sequence 46, Appl
603	5	4.1	426	5	US-09-540-209B-6010	Sequence 6010, Ap	676	5	4.1	497	5	US-09-868-300-10	Sequence 10, Appl
604	5	4.1	427	7	US-60-366-892-38	Sequence 38, Appl	677	5	4.1	498	5	US-09-573-655B-512	Sequence 512, App
605	5	4.1	429	5	US-09-573-655B-1009	Sequence 1009, Ap	678	5	4.1	498	5	US-09-573-655B-593	Sequence 593, App
606	5	4.1	429	5	US-09-743-207-8	Sequence 8, Appl	679	5	4.1	505	5	US-09-573-655B-382	Sequence 382, App
607	5	4.1	432	5	US-09-573-655B-1198	Sequence 1198, Ap	680	5	4.1	507	7	US-60-368-184-3	Sequence 3, Appl
608	5	4.1	433	6	US-10-102-806-463	Sequence 463, App	681	5	4.1	508	7	US-60-366-892-41	Sequence 41, Appl
609	5	4.1	434	1	PCT-US02-07826-73	Sequence 73, Appl	682	5	4.1	510	6	US-10-112-857-15	Sequence 15, Appl
610	5	4.1	434	6	US-10-097-340-73	Sequence 73, Appl	683	5	4.1	511	7	US-60-366-892-42	Sequence 42, Appl

684	5	4.1	514	5	US-09-540-209B-9965	Sequence 9965, Ap	757	607	6	US-10-121-051-344	Sequence 344, App
685	5	4.1	516	1	PCT-US02-09944-525	Sequence 525, App	758	608	5	US-09-540-209B-8786	Sequence 8786, Ap
686	5	4.1	516	5	US-09-573-655B-193	Sequence 193, App	759	613	1	PCT-US02-09944-680	Sequence 680, App
687	5	4.1	516	5	US-09-573-655B-255	Sequence 255, App	760	615	5	US-10-112-178-2	Sequence 2, Appli
688	5	4.1	516	5	US-09-573-655B-1516	Sequence 1516, Ap	761	615	6	US-10-112-178-4	Sequence 4, Appli
689	5	4.1	516	5	US-09-573-655B-1746	Sequence 1746, Ap	762	619	5	US-09-573-655B-2391	Sequence 2391, Ap
690	5	4.1	516	5	US-09-573-655B-1860	Sequence 1860, Ap	763	615	7	US-09-573-655B-264	Sequence 649, App
691	5	4.1	519	5	US-09-540-209B-6278	Sequence 6278, Ap	764	625	7	US-09-573-655B-264	Sequence 21, Appli
692	5	4.1	524	5	US-09-914-543-28	Sequence 28, Appl	765	626	6	US-10-121-235-21	Sequence 5, Appli
693	5	4.1	525	5	US-09-972-211-30	Sequence 30, Appl	766	628	1	PCT-US01-13240-5	Sequence 22, Appl
694	5	4.1	525	5	US-09-972-211-32	Sequence 32, Appl	767	632	6	US-10-041-007-22	Sequence 8469, Ap
695	5	4.1	525	5	US-09-972-211-34	Sequence 34, Appl	768	632	5	US-09-540-209B-7938	Sequence 7938, Ap
696	5	4.1	525	5	US-09-972-211-36	Sequence 36, Appl	769	633	5	US-09-540-209B-7938	Sequence 7938, Ap
697	5	4.1	525	5	US-09-972-211-38	Sequence 38, Appl	770	634	5	US-09-602-777A-272	Sequence 272, App
698	5	4.1	525	5	US-09-972-211-40	Sequence 40, Appl	771	635	5	US-09-540-209B-8038	Sequence 8038, Ap
699	5	4.1	525	5	US-09-972-211-103	Sequence 103, App	772	638	5	US-09-540-209B-7963	Sequence 7963, Ap
700	5	4.1	525	5	US-09-972-211-104	Sequence 104, App	773	640	5	US-09-540-209B-7940	Sequence 7940, Ap
701	5	4.1	525	5	US-09-972-211-105	Sequence 105, App	774	641	5	US-09-573-655B-2022	Sequence 2022, Ap
702	5	4.1	525	5	US-09-540-209B-6761	Sequence 6761, Ap	775	642	5	US-09-602-777A-44	Sequence 44, Appl
703	5	4.1	526	7	US-09-366-892-31	Sequence 31, Appl	776	647	5	US-09-991-262-50	Sequence 50, Appl
704	5	4.1	527	6	US-10-102-806-703	Sequence 703, App	777	649	5	US-09-540-209B-7045	Sequence 7045, Ap
705	5	4.1	529	7	US-09-366-892-57	Sequence 57, Appl	778	650	5	US-09-540-209B-10379	Sequence 10379, A
706	5	4.1	534	1	PCT-US02-06912-7	Sequence 7, Appli	779	650	7	US-09-366-892-294	Sequence 294, App
707	5	4.1	535	7	US-09-366-892-56	Sequence 56, Appl	780	651	7	US-09-366-892-116	Sequence 116, App
708	5	4.1	536	7	US-09-366-892-30	Sequence 30, Appl	781	651	7	US-09-371-420-116	Sequence 116, App
709	5	4.1	537	1	PCT-US02-06912-5	Sequence 5, Appli	782	651	5	US-09-573-655B-1989	Sequence 1989, Ap
710	5	4.1	537	1	PCT-US02-09944-534	Sequence 534, App	783	658	5	US-09-868-677-12	Sequence 12, Appl
711	5	4.1	537	5	US-09-602-777A-46	Sequence 46, Appl	784	667	5	US-09-540-209B-5434	Sequence 5434, Ap
712	5	4.1	540	5	US-09-540-209B-7868	Sequence 7868, Ap	785	669	5	US-09-573-655B-2160	Sequence 2160, Ap
713	5	4.1	540	5	US-09-847-637B-6	Sequence 6, Appli	786	669	6	US-09-573-655B-2198	Sequence 2198, Ap
714	5	4.1	541	6	US-10-100-679-97	Sequence 97, Appl	787	675	5	US-09-573-655B-1087	Sequence 1087, Ap
715	5	4.1	543	1	PCT-US02-09944-685	Sequence 685, App	788	675	5	US-09-991-262-52	Sequence 52, Appl
716	5	4.1	543	7	US-09-366-892-68	Sequence 68, Appl	789	678	6	US-09-895-913A-4	Sequence 4, Appli
717	5	4.1	544	5	US-09-573-655B-1489	Sequence 1489, Ap	790	681	1	PCT-US02-10764-20	Sequence 20, Appl
718	5	4.1	549	5	US-09-573-655B-1671	Sequence 1671, Ap	791	681	1	PCT-US02-10764-24	Sequence 24, Appl
719	5	4.1	554	5	US-09-540-209B-6607	Sequence 6607, Ap	792	681	5	US-09-540-209B-6218	Sequence 6218, Ap
720	5	4.1	556	5	US-09-868-300-2	Sequence 2, Appli	793	683	5	US-09-868-677-10	Sequence 10, Appl
721	5	4.1	553	1	PCT-US02-09785-536	Sequence 536, App	794	683	1	PCT-US02-10764-43	Sequence 43, Appl
722	5	4.1	559	6	US-10-106-275-2	Sequence 2, Appli	795	685	1	PCT-US02-10764-45	Sequence 45, Appl
723	5	4.1	579	5	US-09-990-004A-185	Sequence 185, App	796	685	1	PCT-US02-10764-47	Sequence 47, Appl
724	5	4.1	582	6	US-10-100-679-79	Sequence 79, Appl	797	685	1	PCT-US02-10764-49	Sequence 49, Appl
725	5	4.1	582	6	US-10-100-679-80	Sequence 80, Appl	798	689	1	PCT-US02-07826-221	Sequence 221, App
726	5	4.1	582	6	US-10-100-679-81	Sequence 81, Appl	799	692	1	PCT-US02-10764-16	Sequence 16, Appl
727	5	4.1	584	5	US-09-902-525-33	Sequence 33, Appl	800	692	1	PCT-US02-10764-22	Sequence 22, Appl
728	5	4.1	584	5	US-09-540-209B-7381	Sequence 7381, Ap	801	700	5	US-09-573-655B-1802	Sequence 1802, Ap
729	5	4.1	587	5	US-09-573-655B-811	Sequence 811, App	802	705	6	US-10-106-698-6378	Sequence 6378, Ap
730	5	4.1	590	5	US-09-540-209B-8330	Sequence 8330, Ap	803	705	5	US-09-540-209B-10227	Sequence 10227, A
731	5	4.1	594	5	US-09-573-655B-774	Sequence 774, App	804	716	5	US-09-573-655B-1363	Sequence 1363, Ap
732	5	4.1	594	5	US-09-573-655B-1538	Sequence 1538, Ap	805	716	5	US-09-573-655B-2137	Sequence 2137, Ap
733	5	4.1	604	5	US-09-540-209B-5436	Sequence 5436, Ap	806	722	1	PCT-US02-10812-12	Sequence 12, Appl
734	5	4.1	607	5	US-09-573-655B-1086	Sequence 1086, Ap	807	724	1	PCT-US02-10812-12	Sequence 12, Appl
735	5	4.1	607	6	US-10-121-049-344	Sequence 344, App	808	732	5	US-09-573-655B-2355	Sequence 2355, Ap
736	5	4.1	607	6	US-10-121-050-344	Sequence 344, App	809	732	5	US-09-540-209B-8427	Sequence 8427, Ap
737	5	4.1	607	6	US-10-121-053-344	Sequence 344, App	810	740	5	US-10-108-605-203	Sequence 203, App
738	5	4.1	607	6	US-10-121-043-344	Sequence 344, App	811	745	5	US-09-540-209B-8524	Sequence 8524, Ap
739	5	4.1	607	6	US-10-121-044-344	Sequence 344, App	812	745	7	US-09-366-892-32	Sequence 32, Appl
740	5	4.1	607	6	US-10-121-047-344	Sequence 344, App	813	746	6	US-10-041-007-39	Sequence 39, Appl
741	5	4.1	607	6	US-10-121-054-344	Sequence 344, App	814	752	5	US-09-540-209B-10444	Sequence 10444, A
742	5	4.1	607	6	US-10-121-054-344	Sequence 344, App	815	752	5	US-09-573-655B-925	Sequence 925, App
743	5	4.1	607	6	US-10-121-056-344	Sequence 344, App	816	754	5	US-09-573-655B-1187	Sequence 1187, Ap
744	5	4.1	607	6	US-10-121-057-344	Sequence 344, App	817	754	5	US-09-540-209B-7101	Sequence 7101, Ap
745	5	4.1	607	6	US-10-121-058-344	Sequence 344, App	818	759	5	US-09-540-209B-6609	Sequence 6609, Ap
746	5	4.1	607	6	US-10-121-060-344	Sequence 344, App	819	760	5	US-09-573-655B-1689	Sequence 1689, Ap
747	5	4.1	607	6	US-10-121-063-344	Sequence 344, App	820	769	5	US-09-540-209B-8698	Sequence 8698, Ap
748	5	4.1	607	6	US-10-123-108-344	Sequence 344, App	821	770	5	US-09-540-209B-8700	Sequence 8700, Ap
749	5	4.1	607	6	US-10-123-154-344	Sequence 344, App	822	772	6	US-10-121-032-28	Sequence 28, Appl
750	5	4.1	607	6	US-10-123-156-344	Sequence 344, App	823	773	6	US-10-112-286-2	Sequence 2, Appli
751	5	4.1	607	6	US-10-123-157-344	Sequence 344, App	824	779	5	US-09-573-655B-486	Sequence 486, App
752	5	4.1	607	6	US-10-123-212-344	Sequence 344, App	825	779	5	US-09-573-655B-567	Sequence 567, App
753	5	4.1	607	6	US-10-123-213-344	Sequence 344, App	826	779	5	US-09-573-655B-1321	Sequence 1321, Ap
754	5	4.1	607	6	US-10-123-109-344	Sequence 344, App	827	779	5	US-09-573-655B-1903	Sequence 1903, Ap
755	5	4.1	607	6	US-10-121-041-344	Sequence 344, App	828	786	5	US-09-573-655B-406	Sequence 406, App
756	5	4.1	607	6	US-10-121-045-344	Sequence 344, App	829	786	5	US-09-573-655B-1594	Sequence 1594, Ap

830	4.1	5	789	5	US-09-540-209B-8941	Sequence 8941, Ap	903	4.1	5	941	6	US-10-121-051-464	Sequence 464, Ap
831	4.1	5	795	6	US-10-041-007-37	Sequence 37, Appl	904	4.1	5	944	6	US-10-106-698-6381	Sequence 6381, Ap
832	4.1	5	802	7	US-60-366-892-29	Sequence 29, Appl	905	4.1	5	953	6	US-09-540-209B-8639	Sequence 8639, Ap
833	4.1	5	807	7	US-60-371-507-8	Sequence 8, Appl	906	4.1	5	953	6	US-10-105-931-8	Sequence 8, Appl
834	4.1	5	810	5	US-09-540-209B-6963	Sequence 6963, Ap	907	4.1	5	970	5	US-09-573-655B-1537	Sequence 1537, Ap
835	4.1	5	810	5	US-09-573-655B-1358	Sequence 1358, Ap	908	4.1	5	971	5	US-09-419-291A-2	Sequence 2, Appl
836	4.1	5	812	1	PCT-US02-07826-330	Sequence 330, Ap	909	4.1	5	971	6	US-10-116-048-2	Sequence 2, Appl
837	4.1	5	812	6	US-10-097-340-330	Sequence 330, Ap	910	4.1	5	976	5	US-09-569-528-2	Sequence 2, Appl
838	4.1	5	814	6	US-09-540-209B-9513	Sequence 9513, Ap	911	4.1	5	986	5	US-09-540-209B-10025	Sequence 10025, A
839	4.1	5	814	6	US-10-041-007-35	Sequence 35, Appl	912	4.1	5	996	5	PCT-US02-09288-11	Sequence 11, Appl
840	4.1	5	815	7	US-09-366-892-23	Sequence 23, Appl	913	4.1	5	1005	1	PCT-US02-10133-2	Sequence 2, Appl
841	4.1	5	819	5	US-09-540-209B-8521	Sequence 8521, Ap	914	4.1	5	1005	5	US-09-486-861A-2	Sequence 2, Appl
842	4.1	5	822	7	PCT-US02-10439-2	Sequence 2, Appl	915	4.1	5	1012	6	US-10-109-528-4	Sequence 4, Appl
843	4.1	5	822	7	US-60-366-892-26	Sequence 26, Appl	916	4.1	5	1012	5	US-09-573-655B-1017	Sequence 1017, Ap
844	4.1	5	830	5	US-09-540-209B-8070	Sequence 8070, Ap	917	4.1	5	1013	5	US-10-121-049-198	Sequence 198, Ap
845	4.1	5	832	5	US-09-540-209B-8034	Sequence 8034, Ap	918	4.1	5	1016	6	US-10-121-050-198	Sequence 198, Ap
846	4.1	5	837	5	US-09-688-598B-8	Sequence 8, Appl	919	4.1	5	1024	6	US-10-121-053-198	Sequence 198, Ap
847	4.1	5	837	5	US-09-122-126B-2	Sequence 2, Appl	920	4.1	5	1024	6	US-10-121-053-198	Sequence 198, Ap
848	4.1	5	837	5	US-09-122-126B-2	Sequence 2, Appl	921	4.1	5	1024	6	US-10-121-053-198	Sequence 198, Ap
849	4.1	5	837	5	US-10-006-063A-317	Sequence 317, Ap	922	4.1	5	1024	6	US-10-121-058-198	Sequence 198, Ap
850	4.1	5	837	6	US-10-006-117A-317	Sequence 317, Ap	923	4.1	5	1024	6	US-10-121-060-198	Sequence 198, Ap
851	4.1	5	837	6	US-10-006-130A-317	Sequence 317, Ap	924	4.1	5	1024	6	US-10-121-063-198	Sequence 198, Ap
852	4.1	5	837	6	US-10-006-172A-317	Sequence 317, Ap	925	4.1	5	1024	6	US-10-121-063-198	Sequence 198, Ap
853	4.1	5	837	6	US-10-006-768A-317	Sequence 317, Ap	926	4.1	5	1024	6	US-10-121-057-198	Sequence 198, Ap
854	4.1	5	837	6	US-10-017-527A-317	Sequence 317, Ap	927	4.1	5	1024	6	US-10-121-057-198	Sequence 198, Ap
855	4.1	5	837	6	US-10-017-527A-317	Sequence 317, Ap	928	4.1	5	1024	6	US-10-121-058-198	Sequence 198, Ap
856	4.1	5	837	6	US-10-006-041A-317	Sequence 317, Ap	929	4.1	5	1024	6	US-10-121-060-198	Sequence 198, Ap
857	4.1	5	837	6	US-10-006-818A-317	Sequence 317, Ap	930	4.1	5	1024	6	US-10-121-063-198	Sequence 198, Ap
858	4.1	5	837	6	US-10-012-121A-317	Sequence 317, Ap	931	4.1	5	1024	6	US-10-123-108-198	Sequence 198, Ap
859	4.1	5	837	6	US-10-012-121A-317	Sequence 317, Ap	932	4.1	5	1024	6	US-10-123-108-198	Sequence 198, Ap
860	4.1	5	837	6	US-10-015-386A-317	Sequence 317, Ap	933	4.1	5	1024	6	US-10-123-154-198	Sequence 198, Ap
861	4.1	5	837	6	US-10-015-387A-317	Sequence 317, Ap	934	4.1	5	1024	6	US-10-123-156-198	Sequence 198, Ap
862	4.1	5	839	5	US-09-540-209B-9799	Sequence 9799, Ap	935	4.1	5	1024	6	US-10-123-157-198	Sequence 198, Ap
863	4.1	5	856	5	US-09-573-655B-1008	Sequence 1008, Ap	936	4.1	5	1024	6	US-10-123-213-198	Sequence 198, Ap
864	4.1	5	868	6	US-09-573-655B-1218	Sequence 1218, Ap	937	4.1	5	1024	6	US-10-123-213-198	Sequence 198, Ap
865	4.1	5	873	6	US-10-041-007-4	Sequence 4, Appl	938	4.1	5	1024	6	US-10-123-109-198	Sequence 198, Ap
866	4.1	5	873	6	US-10-041-007-33	Sequence 33, Appl	939	4.1	5	1024	6	US-10-121-041-198	Sequence 198, Ap
867	4.1	5	873	6	US-09-573-655B-941	Sequence 941, Ap	940	4.1	5	1024	6	US-10-121-045-198	Sequence 198, Ap
868	4.1	5	877	5	US-10-067-457-1	Sequence 1, Appl	941	4.1	5	1024	6	US-10-121-046-198	Sequence 198, Ap
869	4.1	5	889	6	US-09-573-655B-1204	Sequence 1204, Ap	942	4.1	5	1024	6	US-10-121-051-198	Sequence 198, Ap
870	4.1	5	892	5	US-09-540-209B-8461	Sequence 8461, Ap	943	4.1	5	1035	5	PCT-US02-08253-236	Sequence 236, Ap
871	4.1	5	893	5	US-09-573-655B-2150	Sequence 2150, Ap	944	4.1	5	1035	5	US-09-573-655B-289	Sequence 289, Ap
872	4.1	5	897	7	US-60-365-264-253	Sequence 253, Ap	945	4.1	5	1035	5	US-09-540-209B-7642	Sequence 7642, Ap
873	4.1	5	903	5	US-09-914-543-4	Sequence 44, Appl	946	4.1	5	1036	1	PCT-US02-07826-83	Sequence 83, Appl
874	4.1	5	911	1	PCT-US02-06415-6	Sequence 6, Appl	947	4.1	5	1042	6	US-10-097-340-83	Sequence 83, Appl
875	4.1	5	911	1	PCT-US02-06415-8	Sequence 8, Appl	948	4.1	5	1045	5	US-09-540-209B-7322	Sequence 7322, Ap
876	4.1	5	922	1	PCT-US02-09444-495	Sequence 495, Ap	949	4.1	5	1050	5	US-09-573-655B-2417	Sequence 2417, Ap
877	4.1	5	924	5	US-09-540-209B-9233	Sequence 9233, Ap	950	4.1	5	1051	1	PCT-US02-07826-79	Sequence 79, Appl
878	4.1	5	941	1	PCT-US02-09785-577	Sequence 577, Ap	951	4.1	5	1051	6	US-10-097-340-79	Sequence 79, Appl
879	4.1	5	941	1	PCT-US02-09785-881	Sequence 881, Ap	952	4.1	5	1052	6	US-09-573-655B-336	Sequence 336, Ap
880	4.1	5	941	5	US-09-991-150-353	Sequence 353, Ap	953	4.1	5	1052	5	US-09-573-655B-654	Sequence 654, Ap
881	4.1	5	941	6	US-10-121-049-464	Sequence 464, Ap	954	4.1	5	1066	5	US-09-540-209B-8040	Sequence 8040, Ap
882	4.1	5	941	6	US-10-121-050-464	Sequence 464, Ap	955	4.1	5	1071	5	US-09-573-655B-2366	Sequence 2366, Ap
883	4.1	5	941	6	US-10-121-053-464	Sequence 464, Ap	956	4.1	5	1084	5	US-09-573-655B-2399	Sequence 2399, Ap
884	4.1	5	941	6	US-10-121-043-464	Sequence 464, Ap	957	4.1	5	1087	5	US-09-540-209B-7962	Sequence 7962, Ap
885	4.1	5	941	6	US-10-121-044-464	Sequence 464, Ap	958	4.1	5	1092	1	PCT-US01-45053-18	Sequence 18, Appl
886	4.1	5	941	6	US-10-121-047-464	Sequence 464, Ap	959	4.1	5	1093	1	PCT-US02-10055-1858	Sequence 1858, Ap
887	4.1	5	941	6	US-10-121-054-464	Sequence 464, Ap	960	4.1	5	1093	6	US-10-102-524-1858	Sequence 1858, Ap
888	4.1	5	941	6	US-10-121-054-464	Sequence 464, Ap	961	4.1	5	1105	5	US-09-573-655B-1300	Sequence 1300, Ap
889	4.1	5	941	6	US-10-121-056-464	Sequence 464, Ap	962	4.1	5	1106	7	US-60-366-892-51	Sequence 51, Appl
890	4.1	5	941	6	US-10-121-057-464	Sequence 464, Ap	963	4.1	5	1110	1	PCT-US02-10421-2921	Sequence 2921, Ap
891	4.1	5	941	6	US-10-121-058-464	Sequence 464, Ap	964	4.1	5	1110	6	US-10-112-699-2921	Sequence 2921, Ap
892	4.1	5	941	6	US-10-121-060-464	Sequence 464, Ap	965	4.1	5	1142	6	US-10-121-988-3	Sequence 3, Appl
893	4.1	5	941	6	US-10-121-063-464	Sequence 464, Ap	966	4.1	5	1151	1	PCT-US02-10055-1857	Sequence 1857, Ap
894	4.1	5	941	6	US-10-123-134-464	Sequence 464, Ap	967	4.1	5	1151	6	US-10-102-524-1857	Sequence 1857, Ap
895	4.1	5	941	6	US-10-123-156-464	Sequence 464, Ap	968	4.1	5	1154	7	US-60-365-264-331	Sequence 331, Ap
896	4.1	5	941	6	US-10-123-157-464	Sequence 464, Ap	969	4.1	5	1163	1	PCT-US02-10824-116	Sequence 116, Ap
897	4.1	5	941	6	US-10-123-212-464	Sequence 464, Ap	970	4.1	5	1163	6	US-10-122-067-4	Sequence 4, Appl
898	4.1	5	941	6	US-10-123-213-464	Sequence 464, Ap	971	4.1	5	1166	7	US-60-369-452-33	Sequence 33, Appl
899	4.1	5	941	6	US-10-123-109-464	Sequence 464, Ap	972	4.1	5	1175	5	US-09-200-650D-7	Sequence 7, Appl
900	4.1	5	941	6	US-10-121-041-464	Sequence 464, Ap	973	4.1	5	1202	1	US-09-540-209B-9066	Sequence 9066, Ap
901	4.1	5	941	6	US-10-121-045-464	Sequence 464, Ap	974	4.1	5	1202	5	PCT-US02-10055-1856	Sequence 1856, Ap
902	4.1	5	941	6	US-10-121-046-464	Sequence 464, Ap	975	4.1	5	1202	6	US-10-102-524-1856	Sequence 1856, Ap

976	5	4.1	1207	5	US-09-573-6558-2161
977	5	4.1	1207	5	US-09-573-6558-2199
978	5	4.1	1207	5	US-09-540-2098-9512
979	5	4.1	1237	6	US-10-108-605-211
980	5	4.1	1251	5	US-09-540-2098-7929
981	5	4.1	1260	5	US-09-715-876-8
982	5	4.1	1266	5	US-09-931-969A-2
983	5	4.1	1302	5	US-09-573-6558-2089
984	5	4.1	1374	6	US-10-121-988-158
985	5	4.1	1381	6	US-10-121-988-95
986	5	4.1	1390	1	PCR-US02-07826-35
987	5	4.1	1390	6	US-10-097-340-35
988	5	4.1	1394	6	US-10-108-605-213
989	5	4.1	1436	5	US-09-573-6558-237
990	5	4.1	1436	5	US-09-573-6558-784
991	5	4.1	1485	5	US-09-573-6558-48
992	5	4.1	1499	1	PCR-US02-07787-67
993	5	4.1	1499	6	US-10-122-067-2
994	5	4.1	1642	5	US-09-573-6558-1841
995	5	4.1	1643	5	US-09-540-2098-5708
996	5	4.1	1651	6	US-10-103-546-10
997	5	4.1	1653	1	PCR-US02-03944-459
998	5	4.1	1686	5	US-09-573-6558-1764
999	5	4.1	1694	5	US-09-863-776-57
1000	5	4.1	1711	1	PCR-US02-03921-1145

ALIGNMENTS

```

RESULT 1
US-09-991-150-359
; Sequence 359, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tsumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Tra
; FILE REFERENCE: Acids Encoding
; FILE REFERENCE: P2730P148
; CURRENT APPLICATION NUMBER: US/09/999
; CURRENT FILING DATE: 2001-11-16
; Prior Application removed - See File
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 359
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-991-150-359

```

Query Match 54.5%; Score 66; DB 5; Length 135;

```

Best Local Similarity   100.0%; Pred. NO. 6.1e-60;      0: Gaps
Matches 66; Conservative 0; Mismatches 0; Indels      0:
QY  1 MRIMLLTAAIFSLAQSGFAGVCKPEQEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGL 60
    |||||
Db   1 MRIMLLTAAIFSLAQSGFAGVCKPEQEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGL 60
    |||||

QY  61 LKALSQ 66
    |||||
Db   61 LKALSQ 66
    |||||

RESULT 2
US-10-119-480-108
; Sequence 108, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 108
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-119-480-108

```

```

Query Match          54.5%; Score 66; DB 6; Length 135;
Best Local Similarity 100.00; Pred. No. 6.le-60;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1 MRIMLLFTAILAFSLAQSGFQAVCKEFQEVVPGGSRKRDPLDYLQRLFKSHSLEGL 60
        |||||
Db      1 MRIMLLFTAILAFSLAQSGFQAVCKEFQEVVPGGSRKRDPLDYLQRLFKSHSLEGL 60

Qy      61 LKALSQ 66
        |||||
Db      61 LKALSQ 66

RESULT      3
PCT-US02-10788-25
; Sequence 25, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT APPLICATION NUMBER: PCT/US02/10788
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens

```


PCT-US02-10788-25

Query Match 5.0%; Score 6; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SLAQSF 19
Db 10 SLAQSF 15

RESULT 4
US-09-710-058A-30
; Sequence 30, Application US/09710058A
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Peelle, Beau
; TITLE OF INVENTION: METHODS AND COMPOSITIONS COMPRISING RENILLA GFP
; FILE REFERENCE: A-68531-1/RMS/CYO
; CURRENT APPLICATION NUMBER: US/09/710,058A
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/164,592
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-710-058A-30

Query Match 5.0%; Score 6; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LLQRLF 51
Db 1 LLQRLF 6

RESULT 5
US-10-043-074-19
; Sequence 19, Application US/10043074
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252-1/DJB/DAV
; CURRENT APPLICATION NUMBER: US/10/043,074
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,827
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/133,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: palmitoylated
; OTHER INFORMATION: sequence
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 269
; PAGES: 27791-27791
; DATE: 1994
US-10-043-074-19

Query Match 5.0%; Score 6; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LLQRLF 51
Db 1 LLQRLF 6

RESULT 6
US-10-103-295-163
; Sequence 163, Application US/10103295
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P2
; CURRENT APPLICATION NUMBER: US/10/103,295
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/US01/29871
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/00911
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/234,925
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-295-163

Query Match 5.0%; Score 6; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SLEGLL 61
Db 26 SLEGLL 31

RESULT 7
US-09-540-209B-7680
; Sequence 7680, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7680
; LENGTH: 84
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-7680

Query Match 5.0%; Score 6; DB 5; Length 84;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 FGAVCK 24
|||||
Db 15 FGAVCK 20

RESULT 8

US-09-990-004A-166
; Sequence 166, Application US/09990004A
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell De
; FILE REFERENCE: 11000.1038c1
; CURRENT APPLICATION NUMBER: US/09/990,004A
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/327,373
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 166
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-990-004A-166

Query Match 5.0%; Score 6; DB 5; Length 96;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GLLKAL 64
|||||
Db 76 GLLKAL 81

RESULT 9

US-10-106-698-8430
; Sequence 8430, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 8430
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-8430

Query Match 5.0%; Score 6; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 LQRLFK 52
|||||
Db 51 LQRLFK 56

RESULT 10

US-09-990-004A-77
; Sequence 77, Application US/09990004A
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell
; FILE REFERENCE: 11000.1038c1
; CURRENT APPLICATION NUMBER: US/09/990,004A
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/327,373
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-990-004A-77

Query Match 5.0%; Score 6; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ILAFSL 15
|||||
Db 75 ILAFSL 80

RESULT 11

PCT-US02-10788-11
; Sequence 11, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies Inhibiting autoimmune disease
; FILE REFERENCE: 1361.005WO1
; CURRENT APPLICATION NUMBER: PCT/US02/10788
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-11

Query Match 5.0%; Score 6; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SLAQSF 19
|||||
Db 52 SLAQSF 57

RESULT 12

US-10-103-295-259
; Sequence 259, Application US/10103295
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P2
; CURRENT APPLICATION NUMBER: US/10/103,295
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/US01/29871

```
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/00911
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/234,925
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 259
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-295-259

Query Match      5.0%; Score 6; DB 6; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SLEGLL 61
Db 85 SLEGLL 90

RESULT 13
US-09-990-004A-76
; Sequence 76, Application US/099900004A
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell De
; FILE REFERENCE: 11000.1038c1
; CURRENT APPLICATION NUMBER: US/09/990,004A
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/327,373
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-990-004A-76

Query Match      5.0%; Score 6; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ILAFSL 15
Db 76 ILAFSL 81

RESULT 14
US-09-540-209B-7831
; Sequence 7831, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
; FILE REFERENCE: 2709,1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
```

```
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7831
; LENGTH: 138
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-7831
```

```
Query Match      5.0%; Score 6; DB 5; Length 138;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 LEFTAIL 11
Db 87 LEFTAIL 92
```

```
RESULT 15
US-10-102-806-795
; Sequence 795, Application US/10102806
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 795
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (19)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (54)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (64)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
```

LOCATION: (71)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (76)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (83)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (87)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (88)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (89)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (93)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (100)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (107)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (110)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (112)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (117)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (127)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (136)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-795

Query Match 5.0%; Score 6; DB 6; Length 144;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GLKAL 64
Db 101 GLKAL 106

Search completed: May 3, 2002, 16:40:05
Job time: 73 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:20:43 ; Search time 23.81 Seconds
(without alignments)
376.433 Million cell updates/sec

Title: US-09-852-659-85

Perfect score: 613

Sequence: 1 MRIMLLFTAILAFSLAQSGF.....DVNQENVPFGLKLYPPRAE 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	610	99.5	121	19 AAW75212	Human secreted pro
2	610	99.5	121	20 AAW97213	A human zneurokl p
3	610	99.5	121	20 AAW74413	HPMB091 protein se
4	610	99.5	121	22 AAB82380	Human neurokinin B
5	609	99.3	121	19 AAW52228	Human secreted pro
6	592.5	96.7	122	20 AAW96144	Human preprotachyk
7	487	79.4	135	21 AAB33445	Human PRO1155 prot
8	487	79.4	135	21 AAB66739	Membrane-bound pro
9	487	79.4	135	22 AAB65262	Human PRO1155 (UNQ
10	407.5	66.5	126	20 AAW96145	Bovine preprotachy
11	344.5	56.2	116	20 AAW96146	Rat preprotachykin

12	261.5	42.7	92	20	AAW75214	A murine homologue
13	247	40.3	51	20	AAW12634	Human 5' EST seque
14	190	31.0	36	19	AAW75249	Fragment of human
15	190	31.0	39	19	AAW74414	HPMB091 protein se
16	77	12.6	15	19	AAW75250	Fragment of human
17	75.5	12.3	195	22	AAW50444	C glutamicum prote
18	71.5	11.7	597	21	AAW52527	Arabidopsis thalia
19	71.5	11.7	598	21	AAW52527	Arabidopsis thalia
20	71.5	11.7	602	21	AAW52527	Arabidopsis thalia
21	71.5	11.7	604	21	AAW52526	Arabidopsis thalia
22	69	11.3	863	13	AAW22357	Carrot aspartokina
23	69	11.3	863	13	AAW22357	Carrot aspartokina
24	68.5	11.2	653	22	AAW75440	Human protein sequ
25	68.5	11.2	704	22	AAB93188	Human protein sequ
26	68	11.1	571	21	AAB92702	Arabidopsis thalia
27	68	11.1	778	21	AAG30502	Arabidopsis thalia
28	68	11.1	808	21	AAG30501	Arabidopsis thalia
29	67.5	11.0	382	17	AAG30500	Human mucosal addr
30	67.5	11.0	382	18	AAW05322	Human MadCAM-1 pro
31	66.5	10.8	2034	20	AAW02069	Human activated ca
32	66.5	10.8	2353	20	AAW06300	Human activated ca
33	66.5	10.8	2353	20	AAW06298	Human activated ca
34	66	10.8	156	22	AAW06299	Human gastric canc
35	66	10.8	343	19	AAB63675	C. heterotrophus
36	65.5	10.7	911	12	AAW42448	Human erythrocyte
37	65.5	10.7	911	12	AAW15355	A. tigrinum AEI pr
38	65.5	10.7	911	22	AAW90263	Human erythrocyte
39	64.5	10.5	647	18	AAB46914	Human cyclin D1-hu
40	64.5	10.5	647	18	AAW00926	Human cyclin D1-hu
41	64.5	10.5	705	18	AAW74575	Human cyclin D1-cy
42	64.5	10.5	705	19	AAW18573	Human cyclin D1-hu
43	64.5	10.5	1005	20	AAW74574	Human cyclin D1-cy
44	64.5	10.5	1374	19	AAW93955	Human 53BP2 protei
45	64	10.4	562	21	AAW69753	Herpes simplex vir
					Arabidopsis thalia	

ALIGNMENTS

RESULT 1
AAW75212
ID AAW75212 standard; Protein; 121 AA.
XX
AC AAW75212;
DT 29-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 17 clone HPMBQ91.
XX
Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
XX WO9840483-A2.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-US04858.
XX
XX 19-DEC-1997; 97US-0068368.
XX
XX 14-MAR-1997; 97US-0040710.
XX
XX 14-MAR-1997; 97US-0040762.
XX
XX 30-MAY-1997; 97US-0048100.
XX
XX 30-MAY-1997; 97US-0048189.
XX
XX 30-MAY-1997; 97US-0048357.
XX
XX 30-MAY-1997; 97US-0050934.

PR 06-JUN-1997; 97US-0048970.
 PR 05-SEP-1997; 97US-00577765.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
 PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
 PI Wei YF, Young PE, Zeng Z;
 XX
 DR WPI; 1998-520811/44.
 DR N-PSDB; AAV34302.
 XX
 PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
 PT used to develop products for the diagnosis and treatment of e.g.
 PT inflammation, cancers, CNS disorders or immune system disorders
 XX
 PS Claim 1; Page 162-163; 201pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAV34277) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 28 novel genes and their fragments (nucleic
 CC acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 28
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV34286 for described uses).
 XX
 SQ Sequence 121 AA;

Query Match 99.5%; Score 610; DB 19; Length 121;
 Best Local Similarity 98.3%; Pred. No. 1.6e-65;
 Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MRIMLLFTAILAFSLAQSGFVAVCKEPEQEEVPGGSKRDPDLYQLLORLFKSHSSLEGL 60
 DB 1 mrimllftailafslagsfavgckepqeevpggskrdpdyqlqlrlfkshsslegl 60
 QY 61 LKALSOXSTDPKSTSPKRDMDHDFVGMGRSVQPDPTDYNQENVPFSFGILKYPRA 120
 DB 61 lkalsqastdpkestspkrdmdhdfvglmgrsvqpdptdvnqenvpfsfgilkyppra 120
 QY 121 E 121
 DB 121 e 121

RESULT 2
 AAW97213
 ID AAW97213 standard; Protein; 121 AA.
 AC AAW97213;
 XX
 DT 07-MAY-1999 (first entry)
 XX
 DE A human zneurokl polypeptide.
 XX
 KW Human; zneurokl; neurokinin B; prohormone convertase; cell growth;
 KW modulation; inflammation; noinception; emesis; contraction;
 KW hormone secretion; DNA synthesis; inositol phosphate turnover;
 KW arachidonate release; phospholipase-C activation; gastric emptying;
 KW human neutrophil activation; ADCC capability;
 KW superoxide anion production; gene therapy.
 OS Homo sapiens.
 XX
 PN WO9855612-A1.

XX 10-DEC-1998.
 XX 28-MAY-1998; 98WO-US10842.
 XX
 PR 02-JUN-1997; 97US-0048290.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO;
 XX
 DR WPI; 1999-070268/06.
 DR N-PSDB; AAX15447.
 XX
 PT New isolated neurokinin polypeptides, zneurokl - used to develop
 PT products for modulating e.g. inflammation, noinception, emesis,
 PT muscle contraction, hormone secretion, DNA synthesis or cell growth
 XX
 PS Claim 3; Page 76-77; 100pp; English.
 XX
 CC The present sequence represents a human zneurokl polypeptide. The
 CC polypeptide releases a neurokinin B polypeptide in the presence
 CC of a prohormone convertase capable of cleaving dibasic amino
 CC acids. The zneurokl polypeptides can be used for modulating inflammation,
 CC noinception or emesis. The polypeptides, fragments, fusion proteins,
 CC agonists, antagonists or antibodies may also modulate contraction,
 CC hormone secretion, DNA synthesis or cell growth, inositol phosphate
 CC turnover, arachidonate release, phospholipase-C activation, gastric
 CC emptying, human neutrophil activation or ADCC capability, or superoxide
 CC anion production. The polynucleotides can also be used for gene therapy.
 CC The products can also be used for detection, diagnosis and screening
 CC assays.
 XX
 SQ Sequence 121 AA;

Query Match 99.5%; Score 610; DB 20; Length 121;
 Best Local Similarity 98.3%; Pred. No. 1.6e-65;
 Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MRIMLLFTAILAFSLAQSGFVAVCKEPEQEEVPGGSKRDPDLYQLLORLFKSHSSLEGL 60
 DB 1 mrimllftailafslagsfavgckepqeevpggskrdpdyqlqlrlfkshsslegl 60
 QY 61 LKALSOXSTDPKSTSPKRDMDHDFVGMGRSVQPDPTDYNQENVPFSFGILKYPRA 120
 DB 61 lkalsqastdpkestspkrdmdhdfvglmgrsvqpdptdvnqenvpfsfgilkyppra 120
 QY 121 E 121
 DB 121 e 121

RESULT 3
 AAW74413
 ID AAW74413 standard; Protein; 121 AA.
 AC AAW74413;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE HPMBQ91 protein sequence.
 XX
 KW HPMBQ91; neurokinin B precursor; neuronal disorder; CNS related disorder;
 KW gastrointestinal disorder; cardiovascular disorder; metabolic disorder;
 KW smooth muscle disorder; inflammatory disorder; cancer; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP892053-A2.
 XX
 PD 20-JAN-1999.
 XX

```
PF 26-JUN-1998; 98EP-0305066.
XX
PR 14-JUL-1997; 97EP-0305215.
XX
PA (HUMA-) HUMAN GENOME SCI.
PA (SMK ) SMITHKLINE BEECHAM PLC.
XX
PI Duckworth DM, Hastings GA, Ruben SM;
XX
DR WPI; 1999-083570/08.
DR N-PSDB; AAX18197.
XX
XX
PT New human neurokinin B precursor (HPMBQ91) polypeptides and
PT polynucleotide - useful as diagnostic reagents and for prevention
PT and treatment of neuronal, metabolic, inflammatory and
PT gastrointestinal disorders, and cancers
XX
PS Claim 11; Page 14-15; 18pp; English.
XX
CC This sequence is the human neurokinin B precursor HPMBQ91 of the
CC invention. HPMBQ91 polypeptides and polynucleotides are useful for
CC diagnosing susceptibility to diseases associated with HPMBQ91 protein
CC imbalance by determining HPMBQ91 polypeptide expression levels. HPMBQ91
CC polypeptides can be used to screen for agonists and antagonists by
CC measuring the binding to HPMBQ91, and observing the stimulation or
CC inhibition of HPMBQ91 function. These can be used in treatment to
CC activate or inhibit HPMBQ91 activity to treat conditions associated with
CC a lack of HPMBQ91 protein. Gene therapy may also be used to affect
CC endogenous HPMBQ91 polypeptide expression. HPMBQ91 antibodies are useful
CC for inducing an immune response to immunise and prevent disease, and for
CC isolating HPMBQ91 clones or purifying the polypeptides by affinity
CC chromatography. HPMBQ91 polypeptides can be administered directly or as a
CC vaccine to inoculate against disease. Diseases diagnosed, prevented and
CC treated include: neuronal disorders; CNS related disorders;
CC gastrointestinal and cardiovascular disorders; metabolic disorders
CC including diabetes and obesity; smooth muscle disorders; inflammatory
CC disorders; and cancers including adenomas, leiomyomas, liposarcomas,
CC melanomas, pulmonary chondroid hamartomas, lung, prostate and breast
CC cancer. The HPMBQ91 polypeptide is also useful for mapping the gene to a
CC chromosome, allowing gene inheritance to be studied through linkage
CC analysis, and tissue localisation studies, for determining HPMBQ91
CC expression patterns.
XX
SQ Sequence 121 AA;

Query Match 99.5%; Score 610; DB 20; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.6e-65;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPQEVVPGGSRKRDPLYLQLLORLFKSHSLEGL 60
DB 1 mrimlftailafslaqsgavckepqeevpgggrskrdpdyqlqlgrfkshslegl 60

QY 61 LKALSQXSTDPKESTSPKRDHDFVGMGRKRSVQPDSPDVGQENVPSEFGLKYPRA 120
DB 61 lkalsqastdpkestspkrdmhdfvglmgrksvqpsdptdvnqenvpsfgilkyppra 120

QY 121 E 121
DB 121 e 121

RESULT 4
AAB82380
ID AAB82380 standard; protein; 121 AA.
XX
AC AAB82380;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human neurokinin B precursor.
XX
```

```
KW Neurokinin B; human; pregnancy; hypertension; pre-eclampsia;
KW diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 81..91
FT FT /label= Neurokinin
XX
PN W0200136979-A2.
XX
PD 25-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-GB04315.
XX
PR 16-NOV-1999; 99GB-0027125.
XX
PA (UTRE-) UNIV READING.
XX
PI Page N, Lowry P;
XX
XX WPI; 2001-355676/37.
XX N-PSDB; AAF90333, AAF90334.
XX
PT Detecting production of the human precursor of neurokinin B by the
PT placenta in pregnancy induced hypertension or pre-eclampsia or related
PT foetal complication
XX
PS Example 1; Fig 1; 63pp; English.
XX
CC The present sequence is that of human neurokinin B (NKB) precursor.
CC The cloning of placental cDNA (see AAF90333) was used to identify
CC the NKB precursor. The precursor is processed to the 10-amino acid
CC NKB peptide. Detection of raised plasma levels of NKB, NKB
CC precursor, its breakdown product or variants at an early stage of
CC pregnancy provide an indication of the likely development of
CC pregnancy induced hypertension or pre-eclampsia. Reduction in the
CC levels of circulating NKB (or reduction of its effects) will
CC ameliorate the adverse effects upon the mother seen in these
CC conditions. Thus, the invention provides methods for predicting or
CC diagnosing pregnancy induced hypertension, pre-eclampsia or
CC related foetal complication based on measuring NKB levels in the
CC blood, and methods for preventing or treating these conditions,
CC e.g. by administering an agent that inhibits the biological
CC effect of NKB, such as an NK1, NK2 or NK3 antagonist.
XX
SQ Sequence 121 AA;

Query Match 99.5%; Score 610; DB 22; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.6e-65;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPQEVVPGGSRKRDPLYLQLLORLFKSHSLEGL 60
DB 1 mrimlftailafslaqsgavckepqeevpgggrskrdpdyqlqlgrfkshslegl 60

QY 61 LKALSQXSTDPKESTSPKRDHDFVGMGRKRSVQPDSPDVGQENVPSEFGLKYPRA 120
DB 61 lkalsqastdpkestspkrdmhdfvglmgrksvqpsdptdvnqenvpsfgilkyppra 120

QY 121 E 121
DB 121 e 121

RESULT 5
AAW75228
ID AAW75228 standard; Protein; 121 AA.
XX
AC AAW75228;
XX
DT 29-JAN-1999 (first entry)
XX
```

XX DE Human secreted protein encoded by gene 17 clone HPMBQ91.
 XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 67 /label= unknown
 FT FT Misc-difference 89 /label= unknown
 FT FT
 XX PN W09840483-A2.
 XX PN 17-SEP-1998.
 XX PD
 XX PD
 XX PF 12-MAR-1998; 98WO-US04858.
 XX PR 19-DEC-1997; 97US-0068368.
 XX PR 14-MAR-1997; 97US-0040710.
 XX PR 14-MAR-1997; 97US-0040762.
 XX PR 30-MAY-1997; 97US-0048100.
 XX PR 30-MAY-1997; 97US-0048189.
 XX PR 30-MAY-1997; 97US-0048357.
 XX PR 30-MAY-1997; 97US-0050934.
 XX PR 06-JUN-1997; 97US-0048970.
 XX PR 05-SEP-1997; 97US-0057765.
 XX PR (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ferlie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
 PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
 PI Wei YF, Young PE, Zeng Z;
 XX WPI; 1998-520811/44.
 DR N-PSDB; AAV34318.
 XX PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
 PT used to develop products for the diagnosis and treatment of e.g.
 PT inflammation, cancers, CNS disorders or immune system disorders
 XX PS Claim 1; Page 175; 201pp; English.
 XX CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAV34277) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 28 novel genes and their fragments (nucleic
 CC acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 28
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV34286 for described uses).
 XX Sequence 121 AA;

Query Match 99.3%; Score 609; DB 19; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e-65;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSFCAVCKEPOEEVYPGGGRKRDPDLYQLQLRFLKSHSLEGL 60
 DB 1 mrImllftailafslaqsfavckepqeevypgggrskrdpdlyqlqlrflkshslegl 60
 QY 61 LKALSOXSSTDPRESTSPEKRDMDHFFVGYMGKRSVQPDSPTDVYNQENVPFGLKYPRA 120
 DB 61 lkalsxsdtpkestspekrdmdhffvgymgkrsvqpdsptdvynqenvpsfglkyppra 120
 QY 121 E 121
 DB 121 e 121
 RESULT 6
 AAW961144
 ID AAW961144 standard; Protein; 122 AA.
 XX AC AAW961144;
 XX DT 27-APR-1999 (first entry)
 XX DE Human preprotachykinin B.
 XX KW Preprotachykinin B; PPT-B; neoplastic disorder;
 KW neurological disorder; Alzheimer's disease; amnesia;
 KW cerebral neoplasms; dementia; multiple sclerosis; Parkinson's disease;
 KW Huntington's disease; Tourette's disorder; angina;
 KW paraneoplastic shock; asthma; cardiovascular shock;
 KW myocardial infarction; migraine.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 104 /label= Leu, Ser or Trp
 FT FT
 XX PN W09857986-A2.
 XX PD 23-DEC-1998.
 XX PF 19-JUN-1998; 98WO-US12855.
 XX PR 19-JUN-1997; 97US-0879995.
 XX PA (INCY-) INCYTE PHARM INC.
 XX PI Hillman JJ, Kaser MR, Lal P;
 XX WPI; 1999-080948/07.
 DR N-PSDB; AAX08906.
 XX PT New human preprotachykinin B - useful for treating neurological
 PT disorders and cancer
 XX PS Claim 1; Page 48-49; 57pp; English.
 XX CC Human preprotachykinin B (PPT-B) can be used to treat a
 CC neurological disorder. Antagonists of PPT-B can also be used in
 CC the treatment of neoplastic disorders. Particular neurological,
 CC disorders include akathisia, Alzheimer's disease, amnesia,
 CC amyotrophic lateral sclerosis, bipolar disorder, catatonia,
 CC cerebral neoplasms, dementia, depression, Down's syndrome, tardive
 CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,
 CC neurofibromatosis, Parkinson's disease, paranoid psychoses,
 CC schizophrenia, and Tourette's disorder. PPT-B or its agonist can
 CC also be used to treat angina, anaphylactic shock, arrhythmias,
 CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,
 CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.
 XX Sequence 122 AA;

ment of
umatoid

history
e,
ed
uses used
d
ain

Query Match	79.48;
Best Local Similarity	95.0%;
Matches	96; Conservative
QY	1 MRIMLLFTAILAFSLAQSGFAGVGV
Db	1 mximllfcaillafslaqsgfagvgs
QY	61 LKALSOXTDPKESTSPKSRDMH
Db	61 lkalsqstdpkestspeksrmdh
RESULT	8
AAV66739	
ID	AAV66739 standard; protein;
XX	XX
AC	AAV66739;

XX 05-APR-2000 (first entry)
XX Membrane-bound protein Prol155.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
XX
XX WO9963088-A2.
XX
XX 09-DEC-1999.
XX
XX 02-JUN-1999; 99WO-US12252.
XX
XX 02-JUN-1998; 98US-0087607.
XX 02-JUN-1998; 98US-0087609.
XX 02-JUN-1998; 98US-0087759.
XX 03-JUN-1998; 98US-0087827.
XX 04-JUN-1998; 98US-0088021.
XX 04-JUN-1998; 98US-0088021.
XX 04-JUN-1998; 98US-0088028.
XX 04-JUN-1998; 98US-0088029.
XX 04-JUN-1998; 98US-0088030.
XX 04-JUN-1998; 98US-0088033.
XX 04-JUN-1998; 98US-0088326.
XX 05-JUN-1998; 98US-0088167.
XX 05-JUN-1998; 98US-0088202.
XX 05-JUN-1998; 98US-0088212.
XX 05-JUN-1998; 98US-0088217.
XX 05-JUN-1998; 98US-0088655.
XX 10-JUN-1998; 98US-0088722.
XX 10-JUN-1998; 98US-0088730.
XX 10-JUN-1998; 98US-0088734.
XX 10-JUN-1998; 98US-0088738.
XX 10-JUN-1998; 98US-0088740.
XX 10-JUN-1998; 98US-0088741.
XX 10-JUN-1998; 98US-0088742.
XX 10-JUN-1998; 98US-0088810.
XX 10-JUN-1998; 98US-0088811.
XX 10-JUN-1998; 98US-0088825.
XX 10-JUN-1998; 98US-0088826.
XX 11-JUN-1998; 98US-0088858.
XX 11-JUN-1998; 98US-0088861.
XX 11-JUN-1998; 98US-0088863.
XX 11-JUN-1998; 98US-0088876.
XX 12-JUN-1998; 98US-0089090.
XX 12-JUN-1998; 98US-0089105.
XX 16-JUN-1998; 98US-0089440.
XX 16-JUN-1998; 98US-0089512.
XX 16-JUN-1998; 98US-0089514.
XX 17-JUN-1998; 98US-0089532.
XX 17-JUN-1998; 98US-0089538.
XX 17-JUN-1998; 98US-0089598.
XX 17-JUN-1998; 98US-0089599.
XX 17-JUN-1998; 98US-0089600.
XX 17-JUN-1998; 98US-0089653.
XX 18-JUN-1998; 98US-0089801.
XX 18-JUN-1998; 98US-0089907.
XX 18-JUN-1998; 98US-0089908.
XX 19-JUN-1998; 98US-0089947.
XX 19-JUN-1998; 98US-0089948.
XX 19-JUN-1998; 98US-0089952.
XX 22-JUN-1998; 98US-0090246.
XX 22-JUN-1998; 98US-0090252.
XX 22-JUN-1998; 98US-0090254.
XX 23-JUN-1998; 98US-0090349.
XX 23-JUN-1998; 98US-0090355.
XX 24-JUN-1998; 98US-0090429.
XX 24-JUN-1998; 98US-0090431.
XX 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096323.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.

```

PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR N-PSDB; AAZ65085.
XX
PT Membrane-bound proteins and related nucleotide sequences
XX claim 12; Fig 254; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence . 135 AA;

Query Match 79.4%; Score 487; DB 21; Length 135;
Best Local Similarity 95.0%; Pred. No. 1.le-50;
Matches 96; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFAGVCKPEQEVVPGGSRKRDPLYOLLQRLFKSHSLGL 60
Db 1 mrimllftailafslaqsfagvckpeqevvpggskrdpdyllqrlfkshsslegl 60

Qy 61 LKALSOXSTDPKSTSPKRDHDFVFGXMGKRSVQPSPT 101
Db 61 lkalsqstdpkstspkrdmhdffvlgmgkrsvqpegkt 101

RESULT 9
AAB65262
ID AAB65262 standard; Protein; 135 AA.
XX
AC AAB65262;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1155 (UNQ585) protein sequence SEQ ID NO:359.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.

```

```

PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX
XX (GETH ) GENENTECH INC.
PA
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrata N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX WPI; 2001-032160/04.
XX N-PSDB; AAF44231.
DR
DR PRO polynucleotides used to produce polypeptides used to target
XX bioactive molecules such as toxins, radiolabels or antibodies, to
XX specific cells, to cause targeted cell death -
XX Claim 12; Fig 254; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 135 AA;

Query Match 79.4%; Score 487; DB 22; Length 135;
Best Local Similarity 95.0%; Pred. No. 1.le-50;
Matches 96; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFAGVCKPEQEVVPGGSRKRDPLYOLLQRLFKSHSLGL 60
Db 1 mrimllftailafslaqsfagvckpeqevvpggskrdpdyllqrlfkshsslegl 60

Qy 61 LKALSOXSTDPKSTSPKRDHDFVFGXMGKRSVQPSPT 101
Db 61 lkalsqstdpkstspkrdmhdffvlgmgkrsvqpegkt 101

RESULT 10

```

AAW96145
ID AAW96145 standard; Protein; 126 AA.

XX AC AAW96145;

XX DT 27-APR-1999 (first entry)

XX DE Bovine preprotachykinin B.

XX KW Preprotachykinin B; PPT-B; neoplastic disorder;

XX KW neurological disorder; Alzheimer's disease; amnesia;

XX KW cerebral neoplasms; dementia; depression; Down's syndrome;

XX KW Huntington's disease; multiple sclerosis; Parkinson's disease;

XX KW paranoid psychoses; schizophrenia; Tourette's disorder; angina;

XX KW anaphylactic shock; asthma; cardiovascular shock;

XX KW myocardial infarction; migraine.

XX OS Bos taurus.

XX PN WO9857986-A2.

XX PD 23-DEC-1998.

XX PF 19-JUN-1998; 98WO-US12855.

XX PR 19-JUN-1997; 97US-0879995.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Hillman JJ, Kaser MR, Lal P;

XX DR WPI; 1999-080948/07.

XX PT New human preprotachykinin B - useful for treating neurological disorders and cancer

XX PS Disclosure; Figure 2; 57pp; English.

XX CC Human preprotachykinin B (AAW96144) (PPT-B) can be used to treat a neurological disorder. Antagonists of PPT-B can also be used in the treatment of neoplastic disorders. Particular neurological, disorders include akathisia, Alzheimer's disease, amnesia,

XX CC amyotrophic lateral sclerosis, bipolar disorder, catatonia, cerebral neoplasms, dementia, depression, Down's syndrome, tardive

XX CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,

XX CC neurofibromatosis, Parkinson's disease, paranoid psychoses,

XX CC schizophrenia, and Tourette's disorder. PPT-B or its agonist can

XX CC also be used to treat angina, anaphylactic shock, arrhythmias,

XX CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,

XX CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.

XX SQ Sequence 126 AA;

Query Match 66.5%; Score 407.5; DB 20; Length 126;

Best Local Similarity 64.3%; Pred. No. 3.7e-41;

Matches 81; Conservative 15; Mismatches 25; Indels 5; Gaps 2;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPOEEVPGGSKRDPDLYQ----LLQRLFKSH-S 55

Db 1 mrstllfavlalsarslgavceeseqvpggghskdsnlqldppslrrlydsrvv 60

QY 56 SLEGLLKALSQSTDPKSTSPKRDMDHFFVCGMGKRSVQDPDPTDVNOENVPSFGILK 115

Db 61 sidgllkmlskasvpgkpslpqkrdmhdfvglmgrknlpdpvdingenipsfgtfk 120

QY 116 YPPRAE 121

Db 121 yppsve 126

RESULT 11

AAW96146

ID AAW96146 standard; Protein; 116 AA.

XX AC AAW96146;

XX DT 27-APR-1999 (first entry)

XX DE Rat preprotachykinin B.

XX KW Preprotachykinin B; PPT-B; neoplastic disorder;

XX KW neurological disorder; Alzheimer's disease; amnesia;

XX KW cerebral neoplasms; dementia; depression; Down's syndrome;

XX KW Huntington's disease; multiple sclerosis; Parkinson's disease;

XX KW paranoid psychoses; schizophrenia; Tourette's disorder; angina;

XX KW anaphylactic shock; asthma; cardiovascular shock;

XX KW myocardial infarction; migraine.

XX OS Rattus rattus.

XX PN WO9857986-A2.

XX PD 23-DEC-1998.

XX PF 19-JUN-1998; 98WO-US12855.

XX PR 19-JUN-1997; 97US-0879995.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Hillman JJ, Kaser MR, Lal P;

XX DR WPI; 1999-080948/07.

XX PT New human preprotachykinin B - useful for treating neurological disorders and cancer

XX PS Disclosure; Figure 2; 57pp; English.

XX CC Human preprotachykinin B (AAW96144) (PPT-B) can be used to treat a neurological disorder. Antagonists of PPT-B can also be used in the treatment of neoplastic disorders. Particular neurological, disorders include akathisia, Alzheimer's disease, amnesia,

XX CC amyotrophic lateral sclerosis, bipolar disorder, catatonia, cerebral neoplasms, dementia, depression, Down's syndrome, tardive

XX CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,

XX CC neurofibromatosis, Parkinson's disease, paranoid psychoses,

XX CC schizophrenia, and Tourette's disorder. PPT-B or its agonist can

XX CC also be used to treat angina, anaphylactic shock, arrhythmias,

XX CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,

XX CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.

XX SQ Sequence 116 AA;

Query Match 56.2%; Score 344.5; DB 20; Length 116;

Best Local Similarity 60.0%; Pred. No. 1.3e-33;

Matches 72; Conservative 16; Mismatches 23; Indels 9; Gaps 3;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPOEEVPGGSKRDPDLY-----QLLQRLFKSHS- 55

Db 1 mrsamlaaavalslawtfgaaceeqe---ggrlskdsdlslppllrrlydsrsl 56

QY 56 SLEGLLKALSQSTDPKSTSPKRDMDHFFVCGMGKRSVQDPDPTDVNOENVPSFGILK 115

Db 57 siegllkvlksasvpgkpslpqkrdmhdfvglmgrknsqdpdpadvveetpsfgvik 116

RESULT 12

AAW97214

ID AAW97214 standard; Protein; 92 AA.

XX AC AAW97214;

XX DT 07-MAY-1999 (first entry)

KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX Homo sapiens.

OS
 PN W09840483-A2.
 XX
 PD
 XX
 PF
 XX
 XX
 XX

17-SEP-1998.

12-MAR-1998; 98WO-US04858.

19-DEC-1997; 97US-0068368.

14-MAR-1997; 97US-0040710.

14-MAR-1997; 97US-0040762.

30-MAY-1997; 97US-0048100.

30-MAY-1997; 97US-0048189.

30-MAY-1997; 97US-0048357.

30-MAY-1997; 97US-0050934.

06-JUN-1997; 97US-0048970.

05-SEP-1997; 97US-0057765.

(HUMA-) HUMAN GENOME SCI INC.

Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
 Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
 Wei YF, Young PE, Zeng Z;

WPI: 1998-520811/44.

N-PSDB; AAV34302.

Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
 used to develop products for the diagnosis and treatment of e.g.
 inflammation, cancers, CNS disorders or immune system disorders

Disclosure; Page 19; 201pp; English.

This sequence represents a fragment of a secreted human protein encoded
 by the nucleic acid molecule designated Gene 17 (AAV34302). The gene
 can be used to generate fusion proteins by linking to the gene to a
 human immunoglobulin Fc portion (e.g. AAV34277) for increasing the
 stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic
 acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)
 which are useful for preventing, treating or ameliorating medical
 conditions e.g. by protein or gene therapy. Also, pathological
 conditions can be diagnosed by determining the amount of the new
 polypeptides in a sample or by determining the presence of mutations in
 the new polynucleotides. Specific uses are described for each of the 28
 polynucleotides, based on which tissues they are most highly expressed in
 (see AAV34286 for described uses).

Sequence 36 AA;

Query Match 31.0%; Score 190; DB 19; Length 36;
 Best Local Similarity 97.2%; Pred. No. 1e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 PEKRDHDFVGVGMKRSVQPSPTDVENQENVPSPG 112
 Db 1 pekrdmhdffvglmgrsvqpsdtdvqenvpsfg 36

RESULT 15

AAW74414

ID AAW74414 standard; Protein; 39 AA.

XX AAW74414;

XX AAW74414;

DT 10-MAY-1999 (first entry)

XX

DE

XX

KW

KW

KW

XX

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

XX

PA

XX

PI

XX

DR

XX

PT

XX

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

HPMBQ91 protein sequence fragment.

HPMBQ91; neurokinin B precursor; neuronal disorder; CNS related disorder;
 gastrointestinal disorder; cardiovascular disorder; metabolic disorder;
 smooth muscle disorder; inflammatory disorder; cancer; gene therapy.

Homo sapiens.

EP892053-A2.

20-JAN-1999.

26-JUN-1998; 98EP-0305066.

14-JUL-1997; 97EP-0305215.

(HUMA-) HUMAN GENOME SCI.

(SMIK) SMITHKLINE BEECHAM PLC.

Duckworth DM, Hastings GA, Ruben SM;
 WPI: 1999-083570/08.

New human neurokinin B precursor (HPMBQ91) polypeptides and
 polynucleotide - useful as diagnostic reagents and for prevention
 and treatment of neuronal, metabolic, inflammatory and
 gastrointestinal disorders, and cancers

Claim 14; Page 15; 18pp; English.

This sequence is the human neurokinin B precursor HPMBQ91 of the
 invention. HPMBQ91 polypeptides and polynucleotides are useful for
 diagnosing susceptibility to diseases associated with HPMBQ91 protein
 imbalance by determining HPMBQ91 polypeptide expression levels. HPMBQ91
 polypeptides can be used to screen for agonists and antagonists by
 measuring the binding to HPMBQ91, and observing the stimulation or
 inhibition of HPMBQ91 function. These can be used in treatment or
 activate or inhibit HPMBQ91 activity to treat conditions associated with
 a lack of HPMBQ91 protein. Gene therapy may also be used to affect
 endogenous HPMBQ91 polypeptide expression. HPMBQ91 antibodies are useful
 for inducing an immune response to immunise and prevent disease, and for
 isolating HPMBQ91 clones or purifying the polypeptides by affinity
 chromatography. HPMBQ91 polypeptides can be administered directly or as a
 vaccine to inoculate against disease. Diseases diagnosed, prevented and
 treated include: neuronal disorders; CNS related disorders;
 gastrointestinal and cardiovascular disorders; metabolic disorders
 including diabetes and obesity; smooth muscle disorders; inflammatory
 disorders; and cancers including adenomas, leiomyomas, liposarcomas,
 melanomas, pulmonary chondroid hamartomas, lung, prostate and breast
 cancer. The HPMBQ91 polypeptide is also useful for mapping the gene to a
 chromosome, allowing gene inheritance to be studied through linkage
 analysis, and tissue localisation studies, for determining HPMBQ91
 expression patterns.

Sequence 39 AA;

Query Match 31.0%; Score 190; DB 20;
 Best Local Similarity 97.4%; Pred. No. 1.1e-15;
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 40 DPDIYQLLQRLFKSHSSLEGLLKALSQXSTDPEKSTPE 78
 Db 1 dpdiylqlrlfkshsslegllkalsqstdpekstpe 39

Search completed: May 3, 2002, 12:24:06

Job time: 203 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:22:33 ; Search time 12.48 Seconds
(without alignments)
218.181 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 613
Sequence: 1 MRMLFTALFSLAQSG.....DVNQENVSPGILKYPRAE 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	592.5	96.7	122	2	US-08-879-995A-1
2	592.5	96.7	122	3	US-09-215-096-1
3	407.5	66.5	126	2	US-08-879-995A-3
4	407.5	66.5	126	3	US-09-215-096-3
5	344.5	56.2	116	2	US-08-879-995A-4
6	344.5	56.2	116	3	US-09-215-096-4
7	69	11.3	863	2	US-08-380-182-19
8	69	11.3	863	3	US-08-380-182-20
9	67.5	11.0	382	3	US-08-582-740-70
10	67.5	11.0	382	4	US-09-109-879-70
11	64.5	10.5	647	2	US-08-770-761A-8
12	64.5	10.5	705	2	US-08-770-761A-7
13	64.5	10.5	1005	2	US-08-935-450-2
14	64	10.4	130	6	5268359-2
15	64	10.4	284	1	US-08-390-858B-36
16	63	10.3	444	3	US-09-221-235-14
17	63	10.3	444	3	US-09-221-928-14
18	63	10.3	444	4	US-09-221-527-14
19	63	10.3	444	4	US-09-221-236-14
20	63	10.3	444	4	US-09-221-416-14
21	63	10.3	444	4	US-09-221-245-14
22	63	10.3	444	4	US-09-163-115-14
23	63	10.3	444	4	US-09-221-528-14
24	63	10.3	444	4	US-09-593-553-14
25	63	10.3	444	4	US-09-221-237-14
26	63	10.3	1360	4	US-09-393-569-2
27	63	10.3	1503	4	US-08-976-255-14

28	61.5	10.0	618	2	US-08-770-761A-3	Sequence 3, Appli
29	61.5	10.0	660	2	US-08-770-761A-2	Sequence 2, Appli
30	61.5	10.0	662	2	US-08-770-761A-5	Sequence 5, Appli
31	61.5	10.0	3118	2	US-08-457-273B-8	Sequence 8, Appli
32	61.5	10.0	3119	1	US-08-246-982A-16	Sequence 16, Appli
33	61.5	10.0	3119	1	US-08-453-265-16	Sequence 16, Appli
34	61.5	10.0	3144	1	US-08-246-982A-6	Sequence 6, Appli
35	61.5	10.0	3144	1	US-08-453-265-6	Sequence 6, Appli
36	61.5	10.0	3144	2	US-08-457-273B-42	Sequence 42, Appli
37	61.5	10.0	3144	3	US-08-556-419-21	Sequence 21, Appli
38	61.5	10.0	3144	4	US-09-041-886-15	Sequence 15, Appli
39	61	10.0	205	3	US-08-989-251-27	Sequence 27, Appli
40	61	10.0	205	3	US-08-989-251-37	Sequence 37, Appli
41	61	10.0	205	3	US-09-340-250-27	Sequence 27, Appli
42	61	10.0	205	3	US-09-340-250-37	Sequence 37, Appli
43	61	10.0	348	2	US-08-953-041-2	Sequence 2, Appli
44	61	10.0	348	4	US-09-159-417-2	Sequence 2, Appli
45	61	10.0	874	2	US-08-456-647B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-879-995A-1
; Sequence 1, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0326 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
US-08-879-995A-1

Query Match 96.7%; Score 592.5; DB 2; Length 122;

```
Best Local Similarity 95.9%; Pred. No. 4.6e-66;
Matches 117; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60

QY 61 LKALSOXSTDPKSTSPKRDMDHFFVGMGKRSVQDPSPTDV-NOENVSPFGILKYPPR 119
Db 61 LKALSOXSTDPKSTSPKRDMDHFFVGMGKRSVQDPSPTDV-NOENVSPFGILKYPPR 120

QY 120 AE 121
Db 121 AE 122

RESULT 3
US-08-879-995A-3
; Sequence 3, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
; US-08-879-995A-3

Query Match 66.5%; Score 407.5; DB 2; Length 126;
Best Local Similarity 64.3%; Pred. No. 4.3e-43;
Matches 81; Conservative 15; Mismatches 25; Indels 5; Gaps 2;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEEYVPGGGRKRDPLDYQLLQRLFKSH-S 55
Db 1 MRSTLLFAVITALLSSARSLGAVCEESQEQVPGGGHKKDSNLYQLPPSLRLRLYDSRVV 60

QY 56 SLEGLLKALSOXSTDPKSTSPKRDMDHFFVGMGKRSVQDPSPTDVNOENVSPFGILK 115
Db 61 SLDGLLMLKSLKASVGVGKPSLPQKRDMDHFFVGLMGKRLQDPTPDVINOENIPSGFTK 120

QY 116 YPPRAE 121
Db 121 YPPSVE 126
```

RESULT 4
US-09-215-096-3
; Sequence 3, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215.096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
US-09-215-096-3

Query Match 66.5%; Score 407.5; DB 3; Length 126;
Best Local Similarity 64.3%; Pred. No. 4.3e-43;
Matches 81; Conservative 15; Mismatches 25; Indels 5; Gaps 2;
Qy 1 MRIMLLFTAILAFSLAQSGAVCKEPQEVVPGGSRKRDPLYQ-----LLQRLFKSH-S 55
Db 1 MRSTLLFAVILASSARISGLAVCEESQEVVPGGSHKSDSLNQLPPSLRLRLYDSRVV 60
Qy 56 SLEGLLKALSOXSTDPKSTSPKEDMDDFFVGMCKRSVQDPTDYNQENVPSPFGILK 115
Db 61 SLDGLLKLMSKASVGPKEPQKRDMDHFFVGLMGKRNQDPTDVPDINQENIPSGFTFK 120
Qy 116 YPPRAE 121
Db 121 YPPSVE 126

RESULT 5
US-08-879-995A-4
; Sequence 4, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 205725
US-08-879-995A-4

Query Match 56.2%; Score 344.5; DB 2; Length 116;
Best Local Similarity 60.0%; Pred. No. 2.5e-35;
Matches 72; Conservative 16; Mismatches 23; Indels 9; Gaps 3;
Qy 1 MRIMLLFTAILAFSLAQSGAVCKEPQEVVPGGSRKRDPLY-----OLLQRLFKSHS- 55
Db 1 MRSAMLFARVLAALSLAWTFGAACEPQEQ---GGRLSKDSDLPLPPPLRLRLYDSRSI 56
Qy 56 SLEGLLKALSOXSTDPKSTSPKEDMDDFFVGMCKRSVQDPTDYNQENVPSPFGILK 115
Db 57 SLEGLLKLMSKASVGPKEPQKRDMDHFFVGLMGKRNQDPTDVPDYNQENVPSPFGVLK 116
RESULT 6
US-09-215-096-4
; Sequence 4, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORMAT:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/380,182
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0226.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-504-6629
TELEFAX: 301-504-5060
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 863 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Daucus carota

US-08-380-182-20

Query Match 11.3%; Score 69; DB 2; Length 863;
Best Local Similarity 31.2%; Pred. No. 6.1;
Matches 29; Conservative 12; Mismatches 42; Indels 10; Gaps 3;
QY 30 VYPGGGRKRDPLQLLQRLFKSHSSLE-GLLKALSOXSTDPKSTSPKRDMDHDFVG 88
DB 185 VYNPAGNOVDYLESEKRLKWFSSQOCOTIVATGFIATSPQNIPTTLKRDGSDFSAA 244
QY 89 XMKG--RSVQPSDPTDVNQENVPFSGILKYPPR 119
DB 245 IMGALLRAGQVTIWDVN-----GVYSADPR 270

RESULT 9
US-08-582-740-70
; Sequence 70, Application US/08582740
; Patent No. 6037324
; GENERAL INFORMATION:
; APPLICANT: Schwender, Charles F.
; APPLICANT: Shroff, Hitesh N.
; TITLE OF INVENTION: Inhibitors of MacCAM-1-Mediated
; TITLE OF INVENTION: Interactions and Methods of Use Therefor
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/582,740
; FILING DATE: 04-JAN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-12
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-582-740-70

Query Match 11.0%; Score 67.5; DB 3; Length 382;
Best Local Similarity 25.4%; Pred. No. 3;
Matches 33; Conservative 15; Mismatches 27; Indels 55; Gaps 7;
QY 11 LAFSL-----AQSFGAVCKPEQEEVPGGGRSKRDPD-LYQLLOR----- 49
DB 147 LSFSLVGGQLEGAQALGPVEQEEEEE--PQG-----DEDVLFRTYRWRRLPPLGTPVP 199
QY 50 -----LFKSHSSLEGLLKALSOXSTDPKSTSPKRDMDHDFVGMKGRSVQ 96
DB 200 PALYCOATMRPLGELSHRQAIPVLH--SPTSPEPDTTSPESPD-----TTS 245
QY 97 PDSPTDVNOE 106
DB 246 PESPDTTSQE 255

RESULT 10
US-09-109-879-70
; Sequence 70, Application US/09109879
; Patent No. 6274556
; GENERAL INFORMATION:
; APPLICANT: Schwender, Charles F.
; APPLICANT: Shroff, Hitesh N.
; TITLE OF INVENTION: INHIBITORS OF MACCAM-1-MEDIATED
; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/109,879
; FILING DATE: 02-JUL-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00291
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/582,740
; FILING DATE: 04-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-12A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-109-879-70

Query Match 11.0%; Score 67.5; DB 4; Length 382;
Best Local Similarity 25.4%; Pred. No. 3;
Matches 33; Conservative 15; Mismatches 27; Indels 55; Gaps 7;
QY 11 LAFSL-----AQSFGAVCKPEQEEVPGGGRSKRDPD-LYQLLOR----- 49
DB 147 LSFSLVGGQLEGAQALGPVEQEEEEE--PQG-----DEDVLFRTYRWRRLPPLGTPVP 199
QY 50 -----LFKSHSSLEGLLKALSOXSTDPKSTSPKRDMDHDFVGMKGRSVQ 96
DB 200 PALYCOATMRPLGELSHRQAIPVLH--SPTSPEPDTTSPESPD-----TTS 245
QY 97 PDSPTDVNOE 106
DB 246 PESPDTTSQE 255

RESULT 11
US-08-770-761A-8
; Sequence 8, Application US/08770761A
; Patent No. 5814503
; GENERAL INFORMATION:
; APPLICANT: Kovacevic, Steven

;; APPLICANT: Otto, Keith A.
;; APPLICANT: Rao, Ramachandra N.
;; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
;; TITLE OF INVENTION: REGULATORY PROTEINS
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Eli Lilly and Company
;; STREET: Lilly Corporate Center/Patent Division
;; CITY: Indianapolis
;; STATE: IN
;; COUNTRY: USA
;; ZIP: 46285
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/770,761A
;; FILING DATE: 19-DEC-1996
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gaylo, Paul J.
;; REGISTRATION NUMBER: 36,808
;; REFERENCE/DOCKET NUMBER: X-10136
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 317-376-0756
;; TELEFAX: 317-277-1917
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 647 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
US-08-770-761A-8

Query Match 10.5%; Score 64.5; DB 2; Length 647;
Best Local Similarity 22.9%; Pred. No. 15;
Matches 30; Conservative 19; Mismatches 37; Indels 45; Gaps 7;

QY 16 AQSFGAVC-----KEPQEEVPPG-----GRSKRDPD-----LYQLLQRLFK--- 52
Db 182 AQTFCALCATDVKFISNPPSMAAGSVAAVQGLNLRSPNNFLSYRLRFLSRVVKCDP 241
QY 53 -----SHSLEGLLKA---LSQXSTDPKSTSPKRDMDHDFVGMKRSVQPD---SPT 101
Db 242 DCLRACQEQIEALLESSLRQAQONMDPKAAEEEEEEEE-----EVDLACTPT 290
QY 102 DVNQENVPSPG 112
Db 291 DVRDVIDASNG 301

RESULT 12
US-08-770-761A-7
; Sequence 7, Application US/08770761A
; Patent No. 5814503
; GENERAL INFORMATION:
; APPLICANT: Kovacevic, Steven
; APPLICANT: Otto, Keith A.
; APPLICANT: Rao, Ramachandra N.
; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
; TITLE OF INVENTION: REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/770,761A
;; FILING DATE: 19-DEC-1996
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gaylo, Paul J.
;; REGISTRATION NUMBER: 36,808
;; REFERENCE/DOCKET NUMBER: X-10136
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 317-376-0756
;; TELEFAX: 317-277-1917
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 705 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
US-08-770-761A-7

Query Match 10.5%; Score 64.5; DB 2; Length 705;
Best Local Similarity 22.9%; Pred. No. 17;
Matches 30; Conservative 19; Mismatches 37; Indels 45; Gaps 7;

QY 16 AQSFGAVC-----KEPQEEVPPG-----GRSKRDPD-----LYQLLQRLFK--- 52
Db 228 AQTFCALCATDVKFISNPPSMAAGSVAAVQGLNLRSPNNFLSYRLRFLSRVVKCDP 287
QY 53 -----SHSLEGLLKA---LSQXSTDPKSTSPKRDMDHDFVGMKRSVQPD---SPT 101
Db 288 DCLRACQEQIEALLESSLRQAQONMDPKAAEEEEEEEE-----EVDLACTPT 336
QY 102 DVNQENVPSPG 112
Db 337 DVRDVIDASMG 347

RESULT 13
US-08-935-450-2
; Sequence 2, Application US/08935450
; Patent No. 5977311
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meifia
; APPLICANT: Schulz, Vincent
; TITLE OF INVENTION: 53BP2 COMPLEXES
; FILE REFERENCE: 7934-054
; CURRENT APPLICATION NUMBER: US/08/935,450
; CURRENT FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1005
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-935-450-2

Query Match 10.5%; Score 64.5; DB 2; Length 1005;
Best Local Similarity 23.9%; Pred. No. 27;
Matches 28; Conservative 13; Mismatches 57; Indels 19; Gaps 3;

QY 6 LFTAILAFSLAQSGAVCKEPQEEVPPGSGGKSRDPLLYQLLQRLFKSHSLEGLLKALS 65
Db 297 LFPQSGASVPSQSTGNALDQVDGCVPLREKEKK-----VRPF-----SMFDAVD 341
QY 66 QXSTDPKSTSPKRDMDHDF-----VGMKRSVQPDPTDVNQENVPSPGILKYPP 118

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:22:53 ; Search time 14.31 Seconds
(without alignments)
644.103 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 613
Sequence: 1 MRIMLLFTAILAFSLAQSGF.....DVNOENVPSGILKYPPRAE 121
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	407.5	66.5	126	A25905	tachykinin B precu
2	364.5	59.5	116	I65342	tachykinin B precu
3	344.5	56.2	116	A43779	neurokinin B precu
4	78.5	12.8	2380	T29551	hypothetical prote
5	77	12.6	1008	T05578	hypothetical prote
6	77	12.6	2211	KRB05	coagulation factor
7	72.5	11.8	1711	T21432	hypothetical prote
8	70	11.4	969	A75634	McrB-related prote
9	69.5	11.3	437	T26767	hypothetical prote
10	69	11.3	921	S35160	aspartate kinase (
11	68.5	11.2	1126	JC4019	DNA mismatch repai
12	68	11.1	293	B44502	nonstructural prot
13	68	11.1	452	T22266	translation initia
14	68	11.1	808	G86185	hypothetical prote
15	68	11.1	906	T47340	hypothetical prote
16	67.5	11.0	578	T48795	origin recognition
17	67.5	11.0	978	RGBY13	regulatory protein
18	67	10.9	823	T16758	hypothetical prote
19	66.5	10.8	929	A32495	rep-1 protein, for
20	66	10.8	211	A42261	heparan sulfate pr
21	66	10.8	343	S34811	mating factor MAT1
22	66	10.8	848	T43810	band 3 anion trans
23	65.5	10.7	839	T45908	hypothetical prote
24	65.5	10.7	911	B3HU	band 3 anion trans
25	65.5	10.7	1880	T18531	tractin - medica
26	65	10.6	282	S46793	vacuolar protein s
27	65	10.6	343	S66173	mating factor MAT-
28	65	10.6	742	D86160	hypothetical prote
29	65	10.6	793	T31655	DNA excision repai

30	64.5	10.5	556	2	T42100	serine/threonine p
31	64.5	10.5	556	2	T36502	serine/threonine p
32	64.5	10.5	773	2	G83816	late competence op
33	64.5	10.5	803	2	B82045	aspartokinase II/h
34	64.5	10.5	890	2	T34243	hypothetical prote
35	64.5	10.5	910	1	S73361	dnar homolog prote
36	64.5	10.5	1374	1	VCBE17	major capsid prote
37	64.5	10.5	2464	1	QRMSPI	microtubule-associ
38	64	10.4	270	2	A72671	hypothetical prote
39	64	10.4	284	2	S17563	RNA-binding protei
40	64	10.4	617	2	S42719	actin-binding prot
41	64	10.4	619	2	T48557	hypothetical prote
42	64	10.4	1119	2	A86340	protein F2D10.24 [
43	64	10.4	1230	2	T30517	complement C3-Q2 -
44	63.5	10.4	198	2	S71964	GTP-binding protei
45	63.5	10.4	222	2	C70041	conserved hypothet

ALIGNMENTS

RESULT 1
A25905
tachykinin B precursor - bovine
N:Alternate names: neuromedin K
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C:Accession: A25905
R:Kotani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
PROC. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986
A:Title: Structure and gene organization of bovine neuromedin K precursor.
A:Reference number: A25905; MUID:86313713
A:Accession: A25905
A:Molecule type: DNA
A:Residues: 1-126 <KOR>
A:Cross-references: GB:M14351; NID:g163587; PIDN:AAA30723.1; PID:g163590
C:Superfamily: neurokinin B precursor
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-126/Product: protachykinin B #status predicted <MAT>

Query Match 66.5%; Score 407.5; DB 2; Length 126;
Best Local Similarity 64.3%; Pred. No. 3e-34; Mismatches 15; Indels 5; Gaps 2;
Matches 81; Conservative 15;

QY	1	MRIMLLFTAILAFSLAQSGFAYCKEPPQEVPGGSRKRDPLQ----	LLQRLFKSH-S	55
DB	1	MRSTLLFAVILALSSARSILGAVCEESQEQVPGGHSKDSNLYQLPPSLRLRLYDSRVV	60	
QY	56	SLEGLLKALSOXSTDPKSTSPKRDMDHFFVGMGKRSVQPSDPTDNNQENVPSFGILK	115	
DB	61	SLDGLLKLMSKASVGPKEPQKRMHDFVGLMGRNLQDPTDPTVDINQENIPSGFTK	120	
QY	116	YPPRAE 121		
DB	121	YPPSVE 126		

RESULT 2
I65342
tachykinin B precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I65342
R:Kako, K.; Munekata, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A:Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and
A:Reference number: I52526
A:Accession: I65342
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-116 <RES>
A:Cross-references: GB:D14423; NID:g407346; PIDN:BAA03316.1; PID:g407347

A:Title: Determination of the disulfide bridges in factor Va heavy chain
A:Reference number: A55979; MUID:95034740
A:Contents: annotation
A:Note: 566-Cys and 617-Cys were shown to have free sulfhydryls
C:Comment: Factor V is activated by thrombin and partially by coagulation
C:Function:
A:Description: acts as a cofactor, with calcium and phospholipid, for the

```

Query Match          11.8%   Score 72.5;   DB 2;   Length 1711;
Best Local Similarity 25.6%   Pred No. 52;
Matches 30;   Conservative 16;   Mismatches 44;   Indels 27;   Gaps 5;

QY  4  MLLFTAILAFS---LAQSFQVCKPEQEEVPPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  28  LWFVFLIMLYSCHFSQILLIFLQRPYDDMAPRGRSKR-----KHPSESG-73

```

Query Match 11.3%; DB 2; Length 437;
Best Local Similarity 27.8%; Pred No. 22;
Matches 22; Conservative 13; Mismatches 33; Indels 11; Gaps 4;
QV 32 PGGG--RSRRDPDY--QLLORLFKSHSLE-----GLLKALSOXSTDPKSTSPKRD 81

Db 237 PGSAVYKHKEDPNLLYNELQSIAGHGKLELKPCKPKLKPKTKLPKPKPKPKPKKH 296
QY 82 MHDFVVGXMGKRSVQDPS 100
Db 297 KHNRTGT-AEKSKKPENP 314

RESULT 10
S35160
aspartate kinase (EC 2.7.2.4) / homoserine dehydrogenase (EC 1.1.1.3) precursor - carrot
C:Species: Daucus carota (carrot)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C:Accession: S35160; S38836
R:Weismann, J.M.; Matthews, B.F.
Plant Mol. Biol. 22, 301-312, 1993
A:Title: Identification and expression of a cDNA from Daucus carota encoding a bifunctional
A:Reference number: S35160; MUID:93283634
A:Accession: S35160
A:Molecule type: mRNA
A:Residues: 1-921 <WEI>
A:Cross-references: EMBL:L11529; NID:9167547; PIDN:AAA16972.1; PID:g464225
A:Accession: S38836
A:Molecule type: protein
A:Residues: 338-358; 405-433, 'S', 435-437; 698-726, 739, 'A', 740-741, 'LGSPS' <WE2>
C:Superfamily: thra bifunctional enzyme; aspartate kinase homology; homoserine dehydroge
C:Keywords: chloroplast; multifunctional enzyme; oxidoreductase; phosphotransferase
F:92-557/Domain: aspartate kinase homology <DKI>
F:560-818/Domain: homoserine dehydrogenase homology <HSD>
F:564-592/Region: beta-alpha-beta NAD(P) nucleotide-binding fold

Query Match 11.3%; Score 69; DB 2; Length 921;
Best Local Similarity 31.2%; Pred. No. 57;
Matches 29; Conservative 12; Mismatches 42; Indels 10; Gaps 3;
QY 30 VVPGGSRKRDPLQLLQRLFKSHSLE-GLLKALSQXSTDPKESTSPKRDHDFVVG 88
Db 243 VVNPAGSNQVDPVLESEKLEKWFSSNQCTIVATGFIATSTQNTPTTLKRGDSFSA 302
QY 89 XMGRK-RSVQPDSTDVNQENVPFSGILKYPPR 119
Db 303 IMGALLRAGQVTIWDVN-----GYVSADPR 328

RESULT 11
JC4019
DNA mismatch repair protein rep-3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 01-Dec-2000
C:Accession: JC4019; B32495; B32495
R:Liu, K.; Niu, L.; Linton, J.P.; Crouse, G.F.
Gene 147, 169-177, 1994
A:Title: Characterization of the mouse Rep-3 gene: Sequence similarities to bacterial an
A:Reference number: JC4019; MUID:95011610
A:Accession: JC4019
A:Molecule type: mRNA
A:Residues: 1-1126 <LIU>
A:Cross-references: GB:I10295
R:Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.;
Mol. Cell. Biol. 9, 3058-3072, 1989
A:Title: Dual bidirectional promoters at the mouse dhfr locus: cloning and characterizat
A:Reference number: A32495; MUID:89384567
A:Accession: B32495
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 47-60 <LIN>
A:Cross-references: GB:M24918; GB:J04244
A:Accession: B32495
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 47-440 <LI2>
A:Cross-references: GB:M24919; NID:g200703; PIDN:AAA40051.1; PID:g200704; GB:J04244

C:Genetics:

A:Gene: Rep-3

A:Introns: 86/2; 159/3; 222/3; 261/3; 301/1; 349/3; 405/2; 443/2; 481/1; 546/2; 650/2
A:Note: gene previously known as Rep-1
C:Keywords: DNA bindingQuery Match 11.2%; Score 68.5; DB 2; Length 1126;
Best Local Similarity 29.3%; Pred. No. 81;
Matches 29; Conservative 8; Mismatches 41; Indels 21; Gaps 5;

QY 32 PGGGRSRKRDPLQLLQRLFKSHSLEGLLKALSQXSTDPKESTSPKRD--MHDFV-- 87

Db 16 PPGRQ-----TVLSRFRFSAGLSR-----SASSTEPAEKMFPTLACNVSHLFRVTE 63

QY 88 GXMGKRSVQDPSPTDVNQENVP-----SFGILKYPPRAE 121

Db 64 GDSRKRSGLNGGPTKKKARKVPEKEENISVASHHPEAK 102

RESULT 12

B44502

nonstructural protein - Chandipura virus (strain I653514)

C:Species: Chandipura virus

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C:Accession: B44502

R:Wasters, P.S.; Banerjee, A.K.

Virology 157, 298-306, 1987

A:Title: Sequences of Chandipura virus N and NS genes: evidence for high mutability o
A:Reference number: A44502; MUID:87151129

A:Accession: B44502

A:Molecule type: mRNA

A:Residues: 1-293 <MAS>

A:Cross-references: GB:M16608; NID:g336043; PIDN:AAA48451.1; PID:g336045

C:Genetics:

A:Gene: NS

C:Superfamily: vesicular stomatitis virus nonstructural protein

C:Keywords: nonstructural protein

Query Match

Best Local Similarity 23.9%; Score 68; DB 1; Length 293;
Matches 17; Conservative 15; Mismatches 37; Indels 2; Gaps 1;

QY 40 DPDLXQLLQRLFKSHSLEGLLKALSQXSTDPKESTSPKRDHDFVVGXMGKRSVQDPS 99

Db 3 DSOLYQALKNYPKQLQDTLDSIENLEDDTKSEFSGSGSPTEGIPSYLAELDECEEDS 62

QY 100 PTDVQNQENVPS 110

Db 63 EED--DDNLPT 71

RESULT 13

S72266

translation initiation factor eIF2B gamma chain - rat

N:Alternate names: guanine nucleotide-exchange protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 31-Mar-2000

C:Accession: S72266

R:Price, N.T.; Kimball, S.R.; Jefferson, L.S.; Proud, C.G.

Biochem. J. 318, 631-636, 1996

A:Title: Cloning of cDNA for the gamma-subunit of mammalian translation initiation fa
A:Reference number: S72265; MUID:96404916

A:Accession: S72266

A:Molecule type: mRNA

A:Residues: 1-452 <PRI>

A:Cross-references: EMBL:U38253; NID:91537014; PIDN:AAC52788.1; PID:gl537015

A:Experimental source: strain Sprague-Dawley

C:Complex: heteropentamer; alpha, beta, gamma, delta and epsilon chain

C:Function:

A:Description: responsible for recycling initiation factor eIF2 to its active GTP-bou
A:Pathway: protein biosynthesis

C;Keywords: blocked amino end; GTP; protein biosynthesis
F;107/Binding site: magnesium (Asp) #status predicted

```

Query Match          11.1%; Score 68; DB 2; Length 452;
Best Local Similarity 27.7%; Pred. No. 32;
Matches 23; Conservative 19; Mismatches 37; Indels 4; Gaps 3;

Qy    40   DPLDYQLLRLFKSHSLEGLKALSOXSTDPKESTSPKKR--DMHDFV-VGMGKRKSQV 96
      | : :::: |::::: :| ||: | |:: | |:: | |:: | |:: |
Db     111  DVALHEVDV-LFRAYDASLAKMRKEQSTPEPVGGKGKKKTVEQDFIGVDSTGRLLF 169

Qy     97   PDSPTDVNQENVPVSFGILKYPPR 119
      : |:::| | |:: | |
Db     170  MANEADLDDEELVIKGSILOKHPR 192
```

RESULT 14

G86185

hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: G86185

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huiziar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.-H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: G86185

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-808 <STO>

A:Cross-references: GB:AE0051172; NID:g2388582; PIDN:AAB71463.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

```

Query Match      11.1%; Score 68; DB 2; Length 808;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 26; Conservative 17; Mismatches 34; Indels 14; Gaps 4;

Qy 10 ILAFSLAQSG-----AVCKEPQEEVVP-----GGRSK--RDPDLYQLQLQRFKS--HS 55
    |||      |      |||      ||      ||      ||      ||      ||      ||
Db 536 IRAFORVTRLGKCDVEARKEMRNDVPVSYSGGGTQKSRKPENLEEILRRLLSLKPD 595

Qy 56 SLEGLLKALSOXSTDPKESTSPKRDHDF 86
    : : | : | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 596 TFOGAIRKAINKEILALLDDSGSGRVDMGMFY 636

```

RESULT 15
T47340
hypothetical protein T21C14.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
C:Accession: T47340
R:Delseny, M.; Berger, C.; Cooke, R.; Gaubier, P.; Grelllet, F.; Laudie, M.; Mewes, H.W.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24462
A:Accession: T47340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-906
A:Cross-references: EMBL:AL138639
A:Experimental source: cultivar Columbia; BAC clone T21C14
C:Genetics:

A; Map position: 3
A; Introns: 90/1; 135/3; 152/3; 152/3; 323/2; 408/3; 432/3; 456/3; 478/3; 500/3; 520/3
A; Note: T21C14.40
C; Superfamily: Arabidopsis thaliana hypothetical protein T21C14.40

Query Match	11.18	Score 68;	DB 2;	Length 906;
Best Local Similarity	28.66;	Pred No. 71;		
Matches 2;	Conservative	10;	Mismatches	29;
			Indels	16;
			Gaps	
QY	33	GGGSKRRDPDLYQLLRFLKSHSLEGL-	-LKALISQXSTDPKESTSPKRDHMDFFVGM	90
Db	295	GGVETKH-----QRPITEGGSSGVVSMESISRISKDPANGTSRPKDVPD-----		340
QY	91	GKRSVQDPDSDPTDVNQEN		107
Db	341	GTRGVSPSKDMGCSGDN		357

Search completed: May 3, 2002, 12:24:47
Job time: 114 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:24:08 ; Search time 11.63 Seconds
(without alignments)
381.466 Million cell updates/sec

Title: US-09-852-659-85

Perfect score: 613

Sequence: 1 MRMLFTAILAFSLAOSFG.....DVNOENVSPGILKYPPRAE 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	407.5	66.5	126	1	TKNK_BOVIN
2	364.5	59.5	116	1	TKNK_MOUSE
3	344.5	56.2	116	1	TKNK_RAT
4	77	12.6	2211	1	FAS_BOVIN
5	72.5	11.8	237	1	AKH1_MOUSE
6	69	11.3	921	1	AKH1_DAUCA
7	68	11.1	293	1	RRPP_CHAV
8	68	11.1	452	1	E2BC_RAT
9	67.5	11.0	978	1	SIR3_YEAST
10	67	10.9	513	1	PIX1_DROME
11	67	10.9	823	1	YRR2_CAEEL
12	66.5	10.8	1091	1	MSH3_MOUSE
13	66.5	10.8	2353	1	CCAH_HUMAN
14	66	10.8	168	1	ARPL_CAEEL
15	66	10.8	201	1	SDC2_RAT
16	66	10.8	343	1	MAT2_COCHE
17	66	10.8	927	1	B3AT_RAT
18	65.5	10.7	911	1	B3AT_HUMAN
19	65	10.6	282	1	PE11_YEAST
20	64.5	10.5	910	1	DNJM_MYCPN
21	64.5	10.5	1005	1	P532_HUMAN
22	64.5	10.5	1374	1	VCAP_HSV11
23	64.5	10.5	2464	1	MAPE_MOUSE
24	64	10.4	617	1	ABP1_SACEX
25	63.5	10.4	198	1	GB11_CANFA
26	63.5	10.4	355	1	CXA5_RAT
27	63.5	10.4	515	1	NCAP_P13B
28	63	10.3	130	1	TKN1_MESAU
29	63	10.3	307	1	CIW7_HUMAN
30	63	10.3	356	1	E2F3_MOUSE
31	63	10.3	465	1	E2F3_HUMAN
32	63	10.3	1270	1	DDX9_HUMAN
33	62.5	10.2	281	1	EF1D_MOUSE

ALIGNMENTS

RESULT 1

ID	TKNK_BOVIN	STANDARD	PRT	126 AA
AC	P08858;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	NEUROKININ B PRECURSOR (NEUROMEDIN K).			
GN	TAC3 OR NKNB OR NKB.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_Taxid=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86313713; PubMed=3462746;			
RA	Kotani H., Hoshimaru M., Nawa H., Nakanishi S.;			
RT	"Structure and gene organization of bovine neuropeptide K precursor."			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:7074-7078(1986).			
CC	-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.			
CC	-!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; M14351; AAA30723.1; JOINED.			
DR	EMBL; M14347; AAA30723.1; JOINED.			
DR	EMBL; M14348; AAA30723.1; JOINED.			
DR	EMBL; M14349; AAA30723.1; JOINED.			
DR	EMBL; M14350; AAA30723.1; JOINED.			
DR	PIR; A25905; A25905.			
DR	InterPro; IPR003635; Neurokinin.			
DR	InterPro; IPR002040; Tachykinin.			
DR	ProDom; PD020370; Neurokinin.1.			
DR	PROSITE; PS00267; TACHYKININ.1.			
DR	Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; signal.			
FT	SIGNAL 1 20 POTENTIAL.			
FT	PEPTIDE 86 95 NEUROKININ B.			
FT	MOD_RES 95 95 AMIDATION (G-96 PROVIDE AMIDE GROUP).			
FT	SEQUENCE 126 AA; 13871 MW; 446EF433498EC059 CRC64;			

Query Match 66.5%; Score 407.5; DB 1; Length 126;
Best Local Similarity 64.3%; Pred. No. 1e-33;
Matches 81; Conservative 15; Mismatches 25; Indels 5; Gaps 2;

RESULT

OC
OY

RP SEQUEN

between
cc

or ser 22

DR InterF

AC Q28107

Eukary

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

FT	REPEAT	1242	1250	7.
FT	REPEAT	1251	1259	8.
FT	REPEAT	1260	1268	9.
FT	REPEAT	1269	1277	10.
FT	REPEAT	1278	1286	11.
FT	REPEAT	1287	1295	12.
FT	REPEAT	1296	1304	13.
FT	REPEAT	1305	1313	14.
FT	REPEAT	1314	1322	15.
FT	REPEAT	1323	1331	16.
FT	REPEAT	1332	1340	17.
FT	REPEAT	1341	1349	18.
FT	REPEAT	1350	1358	19.
FT	REPEAT	1359	1367	20.
FT	REPEAT	1368	1376	21.
FT	REPEAT	1377	1385	22.
FT	REPEAT	1386	1394	23.
FT	REPEAT	1395	1403	24.
FT	REPEAT	1404	1412	25.
FT	REPEAT	1413	1421	26.
FT	REPEAT	1422	1430	27.
FT	REPEAT	1431	1439	28.
FT	REPEAT	1440	1444	29. (PARTIAL).
FT	REPEAT	1445	1453	30.
FT	DOMAIN	1569	1890	F5/8 TYPE A 3.
FT	DOMAIN	1569	1738	PLASTOCYANIN-LIKE 5.
FT	DOMAIN	1748	1890	PLASTOCYANIN-LIKE 6.
FT	DOMAIN	1894	2048	F5/8 TYPE C 1.
FT	DOMAIN	2053	2208	F5/8 TYPE C 2.
FT	SITE	741	742	CLEAVAGE (BY THROMBIN)
FT	SITE	1034	1035	CLEAVAGE (BY THROMBIN)
FT	SITE	1564	1565	CLEAVAGE (BY THROMBIN)
FT	DISULFID	167	193	PROBABLE.
FT	DISULFID	499	525	PROBABLE.
FT	DISULFID	1712	1738	BY SIMILARITY.
FT	DISULFID	1894	2048	BY SIMILARITY.
FT	DISULFID	2053	2208	BY SIMILARITY.
FT	MOD_RES	697	697	SULFATION (POTENTIAL).
FT	MOD_RES	701	701	SULFATION (POTENTIAL).
FT	MOD_RES	730	730	SULFATION (POTENTIAL).
FT	MOD_RES	1513	1513	SULFATION (POTENTIAL).
FT	MOD_RES	1529	1529	SULFATION (POTENTIAL).
FT	MOD_RES	1537	1537	SULFATION (POTENTIAL).
FT	MOD_RES	1541	1541	SULFATION (POTENTIAL).
FT	CARBOHYD	225	225	N-LINKED (GLCNAC. .)
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. .)
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. .)
FT	CARBOHYD	382	382	N-LINKED (GLCNAC. .)
FT	CARBOHYD	460	460	N-LINKED (GLCNAC. .)
FT	CARBOHYD	533	553	N-LINKED (GLCNAC. .)
FT	CARBOHYD	587	587	N-LINKED (GLCNAC. .)
FT	CARBOHYD	745	745	N-LINKED (GLCNAC. .)
FT	CARBOHYD	756	756	N-LINKED (GLCNAC. .)
FT	CARBOHYD	774	774	N-LINKED (GLCNAC. .)
FT	CARBOHYD	780	780	N-LINKED (GLCNAC. .)
FT	CARBOHYD	902	902	N-LINKED (GLCNAC. .)
FT	CARBOHYD	952	952	N-LINKED (GLCNAC. .)
FT	CARBOHYD	964	964	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1044	1044	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1053	1053	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1062	1062	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1071	1071	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1078	1078	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1094	1094	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1451	1451	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1490	1490	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1550	1550	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1690	1690	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1839	1839	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1937	1937	N-LINKED (GLCNAC. .)
FT	CARBOHYD	2196	2196	N-LINKED (GLCNAC. .)
FT	CARBOHYD	587	592	NFTLPA -> T (IN VARIANT 2).
SQ	SEQUENCE	2211	AA; 248981	WM; CBBF90B738667C45 CRC64;

```

Query Match      12.6%; Score 77; DB 1; Length 2211;
Best Local Similarity 28.6%; Pred. No. 14;
Matches 32; Conservative 13; Mismatches 39; Indels 28; Gaps 6;

QY 14 SLAQSGAVCKEP---QEEVPGGGRKRDPLDQ-----LLQRLFKSHSLGGLKAL 64
   ||: | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1269 SLSPDLGQTALSPDPCQESLPDLGQTSLSPDLSPQESLPDLGQTALSPDPQESLPDL 1328

QY 65 SQXSTDP---KESTPEKRDMDHFFVGXMGKRSVQDPTDYNQENV-PSFG 112
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1329 GQTALSPDPQESLSPD-----LGQTSLSLSP-----DLGQESLSPDLG 1365

RESULT 5
HK31_MOUSE
ID HK31_MOUSE STANDARD; PRT; 237 AA.
AC P97436; O09087;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HOMEOBOX PROTEIN NKX-3.1.
GN NKX3A OR NKX-3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=97112961; PubMed=8943214;
RA Biebrich C.J., Fujita K., He W.-W., Jay G.;
RT "Prostate-specific and androgen-dependent expression of a novel
RT homeobox gene.";
RL J. Biol. Chem. 271:31779-31782(1996).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=SWISS WEBSTER;
RX MEDLINE=97287410; PubMed=9142502;
RA Sciavolino P.J., Abrams E.W., Yang L., Austenberg L.P., Shen M.M.,
RA Abate-Shen C.;
RT "Tissue-specific expression of murine Nkx3.1 in the male urogenital
RT system.";
RL Dev. Dyn. 209:127-138(1997).
CC -!- FUNCTION: MAY FUNCTION IN THE GROWTH AND DEVELOPMENT OF THE
CC PROSTATE AND/OR OTHER TISSUES OF THE MALE UROGENITAL SYSTEM AND
CC MAY PLAY A ROLE IN SEXUALLY DIMORPHIC AS WELL AS NON-SEXUALLY
CC DIMORPHIC ORGANOGENESIS. MAY FUNCTION AS A TRANSCRIPTION FACTOR
CC AND PLAY A PROMINENT ROLE BOTH IN THE INITIATION OF PROSTATE
CC DEVELOPMENT AND IN THE MAINTENANCE OF THE DIFFERENTIATED STATE OF
CC PROSTATIC EPITHELIAL CELLS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE MALE UROGENITAL SYSTEM,
CC INCLUDING THE TESTIS, SEMINAL VESICLE, AND THE PROSTATE AND ALSO
CC IN THE DORSAL AORTA AND KIDNEY. EXPRESSION IS ELEVATED IN SEXUALLY
CC MATURE MALES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE MALE UROGENITAL SYSTEM
CC DURING LATE EMBRYOGENESIS AND ADULTHOOD. AT DAY 14.5, EXPRESSED IN
CC THE DEVELOPING UROGENITAL SINUS, AND AT DAY 17.5 IN THE VENTRAL
CC PROSTATIC BUDS. FOUND IN THE DEVELOPING TESTIS AT DAYS 14.5 AND
CC 17.5 OF GESTATION, AND ALSO EXPRESSED AT DAY 14.5 IN THE
CC ENDOTHELIAL CELLS THAT LINE THE DORSAL AORTA WHICH ARE IN
CC PROXIMITY TO THE DEVELOPING METANEPHRIC KIDNEYS.
CC -!- INDUCTION: STIMULATED BY ANDROGEN.
CC -!- SIMILARITY: BELONGS TO THE NK-3 FAMILY OF HOMEOBOX PROTEINS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; L11529; AAA16972.1; -

```

```

or send an email to license@isb-sib.ch).
CC
CC EMBL; U73460; AAC52956.1; -
CC EMBL; U88542; AAB58025.1; -
DR HSSP; P23441; 1FTT.
DR MGD; MGI:97352; Nkx3-1.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PRO0024; HOMEOBOX.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein.
FT DNA_BIND 125 184 HOMEOBOX.
SQ SEQUENCE 237 AA; 26824 MW; 4B074387F3BA1223 CRC64;

Query Match      11.8%; Score 72.5; DB 1; Length 237;
Best Local Similarity 27.3%; Pred. No. 3.4;
Matches 24; Conservative 10; Mismatches 35; Indels 19; Gaps 3;

QY 25 EPOEEVVGGR-----SKRDPDLYQLQRLFKSHSLGGLKALSQXSTDPKEST 75
   ||: | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 EPREPRVEAGGRSFWAAPPTQSKRLTSF--LIQDILDRARHGHSNGSPDPDRDS 63

QY 76 SPEKRDMDHDFVGXMGKRSVQDPTDV 103
   || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 APEP-----DKAGRGVAPEDPPSI 83

RESULT 6
AKH_DAUCA
ID AKH_DAUCA STANDARD; PRT; 921 AA.
AC P37142;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 20-OCT-2001 (Rel. 40, Last annotation update)
DE BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE DEHYDROGENASE, CHLOROPLAST
DE PRECURSOR (AK-HD) (AK-HSDH) [INCLUDES: ASPARTOKINASE (EC 2.7.2.4);
DE HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)] (FRAGMENT).
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93283634; PubMed=8507831;
RA Weismann J.M., Matthews B.F.;
RT "Identification and expression of a cDNA from Daucus carota encoding
RT a bifunctional aspartokinase-homoserine dehydrogenase.";
RL Plant Mol. Biol. 22:301-312(1993).
CC -!- CATALYTIC ACTIVITY: L-HOMOSERINE + NAD(P)(+) = L-ASPARTATE
CC BETA-SEMIALDEHYDE + NAD(P)H.
CC -!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
CC ASPARTATE.
CC -!- PATHWAY: CATALYZES 2 NONCONSECUTIVE REACTIONS IN THE COMMON
CC BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS,
CC TO MET, AND TO THR AND ILE.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
CC ASPARTOKINASE FAMILY.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
CC HOMOSERINE DEHYDROGENASE FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; L11529; AAA16972.1; -

```



```

RESULT 9
SIR3_YEAST
ID SIR3_YEAST STANDARD: PRT; 978 AA.
AC P06701;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE REGULATORY PROTEIN SIR3 (SILENT INFORMATION REGULATOR 3).
GN SIR3 OR STE8 OR MAR2 OR CMT1 OR YLR442C OR L9753.10.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85126876; PubMed=6098447;
RA Shore D., Squire M., Nasmith K.A.;
RT "Characterization of two genes required for the position-effect
RL control of yeast mating-type genes.";
RN EMBO J. 3:2817-2823(1984).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Favello A., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Kucaba T., Fullston L., Gattung S., Greco T., Kirsten J.,
RA Johnson D., Johnson L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Taich A., Trevasakis E., Vignati D.,
RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE PROTEINS SIR1 THROUGH SIR4 CONTROL THE EXPRESSION OF
CC MATING TYPE GENES RESIDENT AT LOCI OF EITHER END OF CHROMOSOME
CC III. SIR3 AND SIR4 ASSOCIATE WITH THE C-TERMINUS OF RAPI TO FORM A
CC DNA-BINDING COMPLEX THAT INITIATES THE REPRESSION AT THE HM LOCI
CC AND TELOMERES.
CC -1- SUBUNIT: INTERACTS WITH RAPI C-TERMINUS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X01420; CAA25668.1; -
CC EMBL; U21094; AAB67522.1; -
CC PIR; S05892; RGYI3.
CC SGD; S0004434; SIR3.
CC InterPro: IPR001025; BAH.
CC Pfam; PF01426; BAH; 1.
CC SMART; SM00439; BAH; 1.
CC Transcription regulation; Repressor; DNA-binding; Nuclear protein.
CC KW CONFLICT 331 331 P -> S (IN REF. 1).
CC CONFLICT 335 335 T -> P (IN REF. 1).
CC CONFLICT 405 405 S -> G (IN REF. 1).
CC CONFLICT 421 421 K -> Q (IN REF. 1).
CC CONFLICT 429 430 NE -> KK (IN REF. 1).
CC CONFLICT 497 497 L -> V (IN REF. 1).
CC CONFLICT 497 587 Q -> R (IN REF. 1).
CC CONFLICT 587 597 I -> V (IN REF. 1).
CC CONFLICT 597 597 Q -> D (IN REF. 1).
CC CONFLICT 669 669 E -> G (IN REF. 1).
CC CONFLICT 704 704 R -> S (IN REF. 1).
CC CONFLICT 712 712 S -> T (IN REF. 1).
CC CONFLICT 726 726 D -> N (IN REF. 1).
CC CONFLICT 828 828 L -> F (IN REF. 1).
CC CONFLICT 830 830 V -> F (IN REF. 1).
CC CONFLICT 925 925 Q -> K (IN REF. 1).
CC SEQUENCE 978 AA; 111359 MW; CA2503D7645397AC CRC64;

Query Match 11.0%; Score 67.5; DB 1; Length 978;
Best Local Similarity 23.2%; Pred. No. 51; Mismatches 17; Gaps 4;
Matches 23; Conservative 17; Indels 23; Gaps 4;

OY 23 CKEPQEVVPGGSRKRDPLDYLQRLFKSH-SLEGLLKALQSXSTDPKSTSPKRD 81
DB 177 CEPTAEKFPV-----IDFIQIRRVKEMEPKQSDYLKRVSV-----PVSGQKTRQV 224
OY 82 MHDFVGVNMGKR-----SVQPSPTDVNQNVP 110
DB 225 MHKMGVERSSRLAKPKSMKKIKIEPSADDDVNNNGNIPS 263

RESULT 10
PIXI_DROME
ID PIXI_DROME STANDARD: PRT; 513 AA.
AC O18400;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PITUITARY HOMEOBOX 1 HOMOLOG (D-PTX1).
GN PTX1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=98092108; PubMed=9431811;
RA Vorbruegg G., Constien R., Zillian O., Wimmer E.A., Dowe G.,
RA Taubert H., Noll M., Jaekle H.;
RT "Embryonic expression and characterization of a Ptx1 homolog in
RT Drosophila.";
RL Mech. Dev. 68:139-147(1997).
CC -1- FUNCTION: MIGHT CONTROL PHYSIOLOGICAL CELL FUNCTIONS THAN PATTERN
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE POSTERIOR REGION OF
CC THE BLASTODERM EMBRYO. IN LATER STAGES OF EMBRYONIC DEVELOPMENT,
CC DETECTED IN THE POSTERIOR PORTION OF THE MIDGUT, IN THE
CC DEVELOPING MALPIGHIAN TUBULES, IN A SUBSET OF VENTRAL SOMATIC
CC MUSCLES, IN THE DEVELOPING CNS AND IN BOLWIG'S ORGAN.
CC -1- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
CC "BICOID" SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ001519; CAA04801.1; -
CC FlyBase; FBgn0020912; ptx1.
CC InterPro: IPR001356; Homeobox.
CC InterPro: IPR003654; OAR_domain.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation; Activator.
CC DOMAIN 119 126 POLY-SER.
CC FT DNA_BIND 268 327 HOMEBOX.
CC SEQUENCE 513 AA; 54804 MW; 3E6B5C19ECEB2E45 CRC64;

```

```
Query Match 10.9%; Score 67; DB 1; Length 513;
Best Local Similarity 27.5%; Pred. No. 28;
Matches 30; Conservative 11; Mismatches 40; Indels 28; Gaps 6;

QY 20 GAVCKEPOEVVGGGRKRDPLQLQLQLF-----KSHSLLEGLLKA----- 63
DB 151 GYSHQPHHTVVP-PHTPKHEP-LEKLSLEFFSWAETGDFRDHSSHTAVANSLDSTH 207
QY 64 LSQXSTDPKESPKRDMHDFVFGXMKRSYQPSDPTDVNOENVPFSG 112
DB 208 LNNFOTSSSTISNRSRDKD-----GNRSV---NETTIKTENISSG 247

RESULT 11
YRR2_CAEEL
ID YRR2_CAEEL STANDARD; PRT; 823 AA.
AC Q09345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 91.1 KDA PROTEIN R144.2 IN CHROMOSOME III.
GN R144.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC STRAIN-BRISTOL N2;
RA Favallo T.;
SEQUENCE FROM N.A.
Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: SOME, TO YEAST PCF11 AND S.POMBE SPAC4G9.04C.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U23515; AAK21453.1; -
DR WormPep; R144.2; CE02032.
KW Hypothetical protein.
SQ SEQUENCE 823 AA; 91142 MW; 18654DB4740FC06A CRC64;

Query Match 10.9%; Score 67; DB 1; Length 823;
Best Local Similarity 26.7%; Pred. No. 47;
Matches 28; Conservative 15; Mismatches 36; Indels 26; Gaps 5;

QY 17 QSGFVCKEPOEVVGGGRKRDPLQLQLRKFSSLSLEGLLKALSOXSTDP---KE 73
DB 205 KSPGTYNKEQVKKP-----KQDP-----LKLFPSSA-----SKTSSSPAGLKR 246
QY 74 STSPKRDHMDFFVFGXMKRSYQPSDPTDVNOENVPFSGILKYPP 118
DB 247 KSPSEHPN-----APIRKKPQPPKQPTAIDEDLRSISLTKKPP 286

RESULT 12
MSH3_MOUSE
ID MSH3_MOUSE STANDARD; PRT; 1091 AA.
AC P13705;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DNA MISMATCH REPAIR PROTEIN MSH3 (REPAIR-3 PROTEIN) (REP-1).
GN MSH3 OR REP-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```



```
FT TRANSMEM 1752 1772 S5-OF REPEAT IV (POTENTIAL).
FT DOMAIN 1773 1835 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1836 1863 S6-OF REPEAT IV (POTENTIAL).
FT DOMAIN 1864 2353 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 520 530 POLY-HIS.
FT DOMAIN 1107 1110 POLY-SER.
FT DOMAIN 1583 1586 POLY-ARG.
FT SITE 378 378 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT SITE 974 974 (BY SIMILARITY).
FT SITE 1504 1504 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT SITE 1504 1504 (BY SIMILARITY).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1466 1466 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 44 44 F -> S (IN REF. 3).
FT CONFLICT 59 59 C -> G (IN REF. 3).
FT CONFLICT 310 311 DV -> EL (IN REF. 3).
FT CONFLICT 684 684 A -> V (IN REF. 3).
FT CONFLICT 1259 1259 V -> E (IN REF. 3).
FT CONFLICT 1265 1265 R -> W (IN REF. 3).
FT CONFLICT 1563 1563 P -> Q (IN REF. 3).
FT CONFLICT 1609 1609 W -> S (IN REF. 3).
FT CONFLICT 1835 1835 P -> L (IN REF. 3).
FT CONFLICT 1847 1847 P -> A (IN REF. 3).
FT CONFLICT 2218 2218 L -> R (IN REF. 3).
FT SEQUENCE 2353 AA; 259166 MW; 115236748BDC0BD8 CRC64;

Query Match 10.8%; Score 66.5; DB 1; Length 2353;
Best Local Similarity 28.3%; Pred. No. 1.7e+02;
Matches 32; Conservative 12; Mismatches 40; Indels 29; Gaps 5;

QY 9 AILAFSLAQSGAVCKPEQEVVPGGSKRDPDLYQLLQRLFKSHS-SLEGLLKALSOX 67
Db 1977 ASLQPLAVSPARSEPLHLSPRG-TARSPSLRLLCRQEAHVTDSEGLKIDS----- 2030

QY 68 STDPKSTSPKRDMDHFFVGXMGKRSVQDPSPTDVNQENVPFSGILKYPPRA 120
Db 2031 ---PRDTLDP-----AEPGEKTPVRP-VTQGGSLQSPPRS 2061

RESULT 14
ARPL_CAEEL STANDARD; PRT; 168 AA.
AC Q9N3B0;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE ARP-LIKE PROTEIN PRECURSOR.
GN Y54G2A.O.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE ARP FAMILY.
CC -!- CAUTION: THE ORIGINALLY PREDICTED SEQUENCE WAS INCORRECT AND
CC MERGED TWO DIFFERENT GENES.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```
CC EMBL; AC024817; AAF59575.1; ALT_SEQ.
DR WormPep; Y54G2A.O; CE25457.
DR InterPro; IPR000886; ER_target.
KW Hypothetical protein; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 168 ARP-LIKE PROTEIN.
FT SEQUENCE 168 AA; 18968 MW; 5A24379E860A6628 CRC64;

Query Match 10.8%; Score 66; DB 1; Length 168;
Best Local Similarity 21.5%; Pred. No. 10;
Matches 23; Conservative 19; Mismatches 33; Indels 32; Gaps 4;

QY 3 IMLETTAILAFSLAQSGAVCKPEQEVVPGGSKRDPDLYQLLQRLFKSHSLEG 59
Db 5 VLLISLVIVASAAPOCEVCKKVDVMAKVPAGDSKPD-----AIGKVIREHC 55

QY 60 LKALSQXSTDPKSTSPKRDMDHFFVGXMGKRSVQDPSPTDVNQE 106
Db 56 -----ETTRNKENKFCFYIGAL-----PESATSIMNE 82

RESULT 15
SDC2_RAT STANDARD; PRT; 201 AA.
AC P34900;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE SYNDSCAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE
DE PROTEIN) (HSPG) (SYND2).
GN SDC2 OR SYND2 OR HSPG1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=92156130; PubMed=1740437;
RA Pierce A., Lyon M., Hampson I., Cowling G.J., Gallagher J.;
RT "Molecular cloning of the major cell surface heparan sulfate
RT proteoglycan from rat liver."
RL J. Biol. Chem. 267:3894-3900(1992).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE SYNDSCAN FAMILY OF INTEGRAL MEMBRANE
CC PROTEOGLYCAN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```
EMBL; M81687; AAA41355.1; -.
PIR; A42261; A42261.
InterPro; IPR003585; 4.1m.
InterPro; IPR001050; Syndecan.
Pfam; PF01034; Syndecan; 1.
SMART; SM00294; 4.1m; 1.
PROSITE; PS00964; SYNDSCAN; 1.
Proteoglycan; Heparan sulfate; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 201 SYNDSCAN-2.
FT DOMAIN 19 144 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 145 169 POTENTIAL.
FT DOMAIN 170 201 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 41 41 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD 53 53 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD 55 55 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
```

FT CARBOHYD 57 57 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT SITE 142 143 CLEAVAGE OF ECTODOMAIN (POTENTIAL).
SQ SEQUENCE 201 AA; 22149 MW; 02E08455754C5E5A CRC64;

Query Match 10.8%; Score 66; DB 1; Length 201;
Best Local Similarity 27.6%; Pred. NO. 12;
Matches 21; Conservative 12; Mismatches 41; Indels 2; Gaps 1;

QY 33 GGGRSKRDPDL--YQLQLFKSHSSLEGLLKALSOXSTDPKSTSPKRDMDHDFVGM 90
Db 58 GAYEDKSPDLTTSQIPRLTSAAPEVETMTLKTQSTPTQTESPEETDKKFEISEA 117

QY 91 GKRSVQPSDPTVYQE 106
Db 118 EEKQDPVKSTDVYTE 133

Search completed: May 3, 2002, 12:27:21
Job time: 193 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:24:28 ; Search time 22.16 Seconds
(without alignments)
798.689 Million cell updates/sec

Title: US-09-852-659-85

Perfect score: 613

Sequence: 1 MRIMLLFTAILAFSLAQSGF.....DVNQNVPSFGILKYPPRAE 121

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL.17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	610	99.5	121	4 Q9UHF0	Q9uhf0 homo sapien
2	357.5	58.3	116	11 Q9QXS9	Q9qxs9 mus musculus
3	78.5	12.8	2380	5 Q22896	Q22896 caenorhabdi
4	77	12.6	1008	10 Q9SB51	Q9sb51 arabidopsis
5	77	12.6	1008	10 Q9SP88	Q9sp88 arabidopsis
6	74.5	12.2	301	5 Q9XV1	Q9xv1 paramedc
7	74	12.1	456	5 Q9V725	Q9v725 drosophila
8	72.5	11.8	208	10 Q9FT99	Q9ft99 arabidopsis
9	72.5	11.8	1711	5 Q45409	Q45409 caenorhabdi
10	72	11.7	392	10 Q9SBR6	Q9sbk6 brassica ra
11	71.5	11.7	597	10 Q9FF55	Q9ff55 arabidopsis
12	71	11.6	172	11 Q9D4S8	Q9d4s8 mus musculus
13	71	11.6	605	2 Q9AH41	Q9ah41 neisseria c
14	70.5	11.5	397	2 Q86938	Q86938 streptomyce
15	70	11.4	645	10 Q9FLQ5	Q9flq5 arabidopsis
16	70	11.4	969	2 Q9RZ15	Q9rzi5 deinococcus
17	69.5	11.3	246	3 Q9C239	Q9c239 neurospora
18	69	11.3	309	5 Q9G924	Q9g924 paramedc
19	69	11.3	463	5 Q9VZ15	Q9vz15 drosophila

Q9x7e2 mycobacteri
Q9v9w5 drosophila
Q9n6u5 drosophila
Q9vte2 drosophila
Q9kj21 pseudomona
Q23052 arabidopsis
Q9m2b1 arabidopsis
Q61048 mus musculu
Q9d0q2 mus musculu
Q9p6v0 neurospora
Q9vcj6 drosophila
Q9be82 macaca fasc
Q9nyy4 homo sapien
Q9y331 homo sapien
Q9rl16 streptomyce
Q919b3 xenopus lae
Q91995 xenopus lae
Q91k31 mus musculu
Q85178 human parvo
Q9eqw6 mus musculu
Q91kn4 mus musculu
Q9nl92 octopus vul
Q91ff3 arabidopsis
Q18465 hirudo medi
Q9vgt6 brachydanio
Q00307 bipolaris s

ALIGNMENTS

RESULT 1

Q9UHF0 PRELIMINARY; PRT; 121 AA.
AC Q9UHF0:
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE NEUROKININ B-LIKE PROTEIN ZNEUROK1.
GN ZNEUROK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sheppard P., Jellinek L., Whitmore T., Blumberg H., Lehner J.,
RA O'Hara P.
RT "Homo sapiens homolog of neurokinin B.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=20322570; PubMed=10866201;
RA Page N.M., Woods R.J., Gardiner S.M., Lomthasong K., Gladwell R.T.,
RA Butlin D.J., Manyonda I.T., Lowry P.J.;
RT "Excessive placental neurokinin B secretion during the third trimester
causes pre-eclampsia.";
RL Nature 405:797-800(2000).
DR EMBL; AF186112; AAF01430.1; -;
DR EMBL; AF216586; AAF76980.1; -;
DR InterPro; IPRO02040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
SQ SEQUENCE 121 AA; 13438 MW; 14C9AFE2EE9EDECA CRC64;

Query Match 99.5%; Score 610; DB 4; Length 121;
Best Local Similarity 98.3%; Pred. No. 5.7e-60;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSGFCAVCCKEPEEVPVGGGSKRDPDLYQLLQRLFKSHSSLEGL 60

Db 1 MRIMLLFTAILAFSLAQSGFCAVCCKEPEEVPVGGGSKRDPDLYQLLQRLFKSHSSLEGL 60

Qy	61	LKALSOXSTDPKSTSPKSRDMHDFVGMGKRSVQDPSPTDVNQENVPSEGLLKYPPRA	120
Db	61	LKALSOASTDPKSTSPKSRDMHDFVGLMGKRSVQDPSPTDVNQENVPSEGLLKYPPRA	120
Qy	121	E 121	
Db	121	E 121	
RESULT	2		
Q9QXS9		PRELIMINARY; PRT; 116 AA.	
ID	Q9QXS9		
AC	Q9QXS9;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	NEUROKININ B-LIKE PROTEIN ZNEUROK1.		
GN	TAC2 OR ZNEUROK1.		
OS	Mus musculus (Mouse).		
GC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RA	Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,		
RA	O'Hara P.;		
RT	"Mus musculus homolog of neurokinin B.";		
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.		
EMBL	AF186116; AF01434.1; -;		
DR	MGD; MGI:98476; Tac2.		
DR	InterPro: IPR002040; Tachykinin.		
DR	PROSITE: PS00267; TACHYKININ; UNKNOWN_1.		
SQ	SEQUENCE 116 AA; 12737 MW; BD4C8B171C2213CC CRC64;		

Query Match	58.3%	Score 357.5	DB 11	Length 116
Best Local Similarity	62.5%	Pred. No. 4.9e-32		
Matches	75	Conservative 15	Mismatches 21	Indels 9
Gaps	3			

QY	1	MRIMLLFTAILAFSLAOSFGAVCKEPOEEVPGGSRKRPDLQ----	LLQRLFKSHS-	55
DB	1	MRSAMLFAAVLALSLAWTFGAVCEPOGQ-----GGRLSKDSLDYQLPSPLLRRLYDSRPV	56	
QY	56	SLEGLLKALSOXSTDPDKRESTSPERKDMHDFVFGXMGKRKSVPQDSPTDQNVQNVPSFGILK	115	
DB	57	SLEGLLKVLSKASVGPKNETSILPQKRDMDHDFVGLMGKRNSQDPDPTDQVEENTPSFGILK	116	

RESULT	3
Q22896	
ID	Q22896
AC	PRELIMINARY;
PR	2380 AA.
DT	01-NOV-1996 (Tremblrel. 01, Created)
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	DE SIMILAR TO TYROSINE-PROTEIN KINASE.
GN	C16D9.2.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC	Rhabditidae; Pelodierinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BRISTOL N2.
RX	MEDLINE=941130718; PubMed=7906398;
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA	Boxfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA	Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA	Lighthning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA	Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,

RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Gattung S., Le T.T.;
RN Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64859; AAB18281.1; -.
DR HSP; P00523; 2PTK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00041; fn3; 3.
DR Pfam: PF00069; pkinase; 2.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 2380 AA; 264939 MW; 88ED3DED8FC952DA CRC64;

```

Query Match      12.8%; Score 78.5; DB 5; Length 2380;
Best Local Similarity 38.6%; Pred. No. 13;
Matches 22; Conservative 8; Mismatches 18; Indels 9; Gaps 3;

Qy      65  SQXSTDPKSTSPKRDWHDFVCGXMKGRSVQDPSTDVNGENVPSPGILKYPRAE 121
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2160  SODSTSSREPPSPSHR-MRDF-----IDTRDLEPPSPHLNQ-----SFGGEFHPYEGE 2207

RESULT      4
Q9SB51
ID Q9SB51 PRELIMINARY; PRT; 1008 AA.
AC A09SB51;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DE HYPOTHETICAL 110.6 KDA PROTEIN.
F22K18.240 OR AT4G24560.
GS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
RA Bevan M., Wedler H., Wedler E., Wambutt R., Hoheisel J., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.

```

RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035356; CAA23007.1; -
DR EMBL; AL161561; CAB79366.1; -
DR InterPro: IPR001394; UCH-2.
DR InterPro: IPR002893; Znf-WYND.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR Pfam; PF01753; zf-WYND; 1.
DR PROSITE; PS0235; UCH_2_3; 1.
KW Hypothetical protein.
SQ SEQUENCE 1008 AA; 110599 MW; F2DF3BD6E9039B9E CRC64;

Query Match 12.6%; Score 77; DB 10; Length 1008;
Best Local Similarity 33.0%; Pred. No. 7;
Matches 29; Conservative 8; Mismatches 41; Indels 10; Gaps 4;
QY 32 PGGRSRKRDPLVQLQLRPFK-----SHSLEGLLKALSOXSTDPKSTSPKRDHMDFF 86
Db 896 PGGRSGNIQSFYSSFRQLKLEEDSASDSSSLFDSNDECSCTDSTSMDFDADF 953
QY 87 VG-XMGKRSVQPD--SPTDVNQENVPF 111
Db 954 FGDRQGRAHGQSTPTSPSSSSSSPPF 981

RESULT 5
Q9FPF8 PRELIMINARY; PRT; 1008 AA.
AC Q9FPF8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UBIQUITIN-SPECIFIC PROTEASE 16.
GN UBP16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20567829; PubMed=11115897;
RA Yan N., Doelling J.H., Falbel T.G., Durski A.M., Vierstra R.D.;
RT "The Ubiquitin-Specific Protease Family from Arabidopsis. AtUBP1 and 2
Are Required for the Resistance to the Amino Acid Analog Canavanine.";
RL Plant Physiol. 124:1828-1843(2000).
DR EMBL; AF302666; AAG42757.1; -
DR InterPro: IPR001394; UCH-2.
DR InterPro: IPR002893; Znf-WYND.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR Pfam; PF01753; zf-WYND; 1.
DR PROSITE; PS0235; UCH_2_3; 1.
KW Protease.
SQ SEQUENCE 1008 AA; 110585 MW; 2BAC6F35ED506DFB CRC64;

Query Match 12.6%; Score 77; DB 10; Length 1008;
Best Local Similarity 33.0%; Pred. No. 7;
Matches 29; Conservative 8; Mismatches 41; Indels 10; Gaps 4;
QY 32 PGGRSRKRDPLVQLQLRPFK-----SHSLEGLLKALSOXSTDPKSTSPKRDHMDFF 86
Db 896 PGGRSGNIQSFYSSFRQLKLEEDSASDSSSLFDSNDECSCTDSTSMDFDADF 953
QY 87 VG-XMGKRSVQPD--SPTDVNQENVPF 111
Db 954 FGDRQGRAHGQSTPTSPSSSSSSPPF 981
RESULT 6

Q9XYV1 PRELIMINARY; PRT; 301 AA.
AC Q9XYV1
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT PROTEIN KINASE CDK2.
GN CDK2.
OS Paramaecium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramaecium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=51S;
RA Zhang H., Berger J.D.;
RT "A novel member of the cyclin-dependent kinase family in Paramaecium
tetraurelia.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF126147; AAD34354.1; -
DR HSSP; P28523; 1A60.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Cyclin; Kinase; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 301 AA; 34675 MW; E839F1A5EA0D5CB5 CRC64;
Query Match 12.2%; Score 74.5; DB 5; Length 301;
Best Local Similarity 29.3%; Pred. No. 3-2;
Matches 34; Conservative 10; Mismatches 45; Indels 27; Gaps 5;
QY 8 TAILAFSLAQSGAVCKEPOEEVVP-----GGRSKRDP-DLYQL-----LQ 48
Db 146 TQIADFGLARAFGLPLKTYTHEVITLWYRAPEILLGORYSTPVDIWSLGCIFAEMAQR 205
QY 49 RLFSKSHSLEGLLKALSOXSTDPKSTSPKRDHMDFFVCGXMGKRSVQPSDPTDVN 104
Db 206 PLPCGSEIDQLPKFKIMGT-PRSTWPGVSTLPDF-----KSTFPKRWPTPTN 253

RESULT 7
Q9V7Z5 PRELIMINARY; PRT; 456 AA.
AC Q9V7Z5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG11395 PROTEIN.
GN CG11395.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,


```
RESULT 10
Q9SBK6
AC Q9SBK6; PRELIMINARY; PRT; 392 AA.
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FLORAL NECTARY-SPECIFIC PROTEIN.
GN NTRI.
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RN SEQUENCE FROM N.A.
RA Song J.T., Seo H.S., Song S.I., Lee J.S., Choi Y.D.;
RT "Characterization of a novel gene expressed specifically in the floral
RL nectarifer of Brassica campestris L. ssp. pekinensis.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF179222; AAF22289.1;
SQ SEQUENCE 392 AA: 43815 MW; 25B78530E93B5757 CRC64;

Query Match 11.7%; Score 72; DB 10; Length 392;
Best Local Similarity 25.7%; Pred. NO. 8.3;
Matches 35; Conservative 18; Mismatches 47; Indels 36; Gaps 8;

QY 10 ILAFSLAQSGFVAVCKPEQEVVPGG-----GRSKRPD-----LYQLLQRLFK 52
DB 207 VVALQFQTFVFLRSSEELVPGGRVLSFLGRSPDPTTESCYQWELLAAQLMSLAK 266
QY 53 SHSLEGLLKALQSXTD-----PKSTSPKRMHDFVFXMGKRSVQ--PDSPTDVNQE 106
DB 267 -----EGITE---EENIDAFNAPYAAPEELKM---AIEKSGFSIDRLSPVDWEGG 315
QY 107 NV--PSFGILKYPPRA 120
DB 316 SISDDSYDIVRFKPEA 331

RESULT 11
Q9FF55
AC Q9FF55; PRELIMINARY; PRT; 597 AA.
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PROTEIN DISULPHIDE ISOMERASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN=COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones.";
RL DNA Res. 4:215-230(1997).
DR EMBL; AB005246; BAB09837.1;
DR InterPro; IPR000886; ER.target.
DR InterPro; IPR000063; Thior.
DR Pfam; PF00085; thior.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Isomerase.
SQ SEQUENCE 597 AA: 66357 MW; 5A8FC7E72AA64B2B CRC64;
```

```
Query Match 11.7%; Score 71.5; DB 10; Length 597;
Best Local Similarity 24.8%; Pred. No. 15;
Matches 27; Conservative 17; Mismatches 30; Indels 35; Gaps 5;

QY 2 RIMLFL--TAILAFS-LAQSGA-----VCKPEQEVVPGG----- 34
DB 4 RVLLFLSLTALLFSAVSPFAASSDDVDRLSLFLDLKEDDVPGLDLSLSSSTGTFDEF 63
QY 35 -GRSKRPDLYQLLQRLFKSHSLGKLLKALQSXTDPKSTSPKRD 82
DB 64 EGGEEDPDY-----NDDDEEGDFSDLGPNPDSPLPTPEIDKDV 105

RESULT 12
Q9D4S8
ID Q9D4S8; PRELIMINARY; PRT; 172 AA.
AC Q9D4S8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE 4930563P03RIK PROTEIN.
GN 4930563P03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21083660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Sato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK016213; BAB30150.1;
DR MGD; MGI:1914905; 4930563P03RIK.
SQ SEQUENCE 172 AA: 19043 MW; E3243D9122FC5811 CRC64;
```

```
Query Match 11.6%; Score 71; DB 11; Length 172;
Best Local Similarity 26.4%; Pred. No. 4;
Matches 32; Conservative 16; Mismatches 55; Indels 18; Gaps 6;

QY 2 RIMLFTAILAFSLAQSGFVAVCKPEQEVVPGGSKRDPDLYQLLQRLFKSHSLGILL 61
DB 3 RIILVVRVAPQHQ-QQMFGEELPESQDGEQPGPARRKQPSMSEAMPLYTLCKEDLESMD 61
QY 62 K----ALQXSTDPK-ESTSPKRDMDHDFVFXMGKRSVQDPS--TDVNQE---NVPSF 111
DB 62 KEVDILGEGSDSDIETKKPKPEDQNEQ-----ERAPKPKRPAPGIRREQVGLPSS 114
QY 112 G 112
DB 115 G 115
```

[illegible]

```

Query Match      11.5%; Score 70.5; DB 2; Length 397;
Best Local Similarity 24.6%; Pred. No. 12;
Matches 29; Conservative 10; Mismatches 50; Indels 29; Gaps 4;

QY 13 FSLAQSGAVCKEPQEEVPGG-----GSRKRDPDLYOLLQRLFKSHSLEGLL 61
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 158 FLLPQ--GVVADEPLNETAPRSATGQVVRYPGRCSAARPTRIAALERLL--AELPRDA 212
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 62 KALSOXSTDPKESTSPKRDWHDFEVCXMGKRVSQVPSPTDVNOENVPSGILKYPPR 119
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 213 AVVSTTGKSSRELYTLDDRQHFYFMVGAAGAA-----TVGLGVALHLPTR 257
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 15
Q9FLQ5
ID Q9FLQ5 PRELIMINARY; PRT; 645 AA.
AC Q9FLQ5;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 5, PL CLONE:MCO15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned pl and PAC clones.";
RL DNA Res. 5:41-54(1998).
DR EMBL; AB010071; BAB08575.1; -.
DR InterPro; IPR000873; AMP-bind.
DR PROSITE; PS00455; AMP_BINDING; UNKNOWN_1.
SQ SEQUENCE 645 AA; 72440 MW; 6A5DC8C9041302F4 CRC64;

Query Match 11.4%; Score 70; DB 10; Length 645;
Best Local Similarity 21.8%; Pred.No. 25;
Matches 31; Conservative 23; Mismatches 62; Indels 26; Gaps

Qy 6 LFTAI--LAFSLAQSGAV-----CKEQEEVVPGGGSKRDPDLYQLLRLEFS 53
||||| : | : | : ||| : | : | : | : | : | : | : | :
Db 499 LFTSLVSLGFVMYEPVLATNDDLSKLFCEKDYVAICQGAWTDKLDDLCCQYIVETM 558
||| : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 54 HSSLLEGLLKALSOXSTDPKESTPEKRDMDHFFVGXMGKRVSOPDSPTDVNQENV---- 108
||| : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 559 LLREEVLRSMKWTEESPSGSETKRKRFKLGIFRGSKERKQTRVPSETQAKSTEPSPR 618
||| : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 109 PSFGIL-----KYPPRAE 121
||| : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 619 QSFSLSFDGKSSLSFKRPPRPE 640

Search completed: May 3, 2002, 12:27:50
Job time: 202 sec

```

Search completed: May 3, 2002, 12:27:50
Job time: 202 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:24:48 ; Search time 24 Seconds
(without alignments)
373.453 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRIMLETTAILAFLAQSG,.....DVNQENVSFGILKYPPRAE 121

Scoring table: OLIGO

Scoring table:

Searched: 522463 seqs, 74073290 residues

Word size :

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A Geneseq 1101:*

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query % Match	Score	Length	DB	ID	Description
1	98.3	119	121	19	AAW75228	Human secreted pro
2	54.5	66	121	19	AAW75212	Human secreted pro
3	54.5	66	121	20	AAW97213	A human neurokri p
4	54.5	66	121	20	AAW74113	HPMBQ91 protein se
5	54.5	66	121	22	AAW82380	Human neurokinin B
6	54.5	66	122	20	AAW96144	Human preprotachyk
7	54.5	66	135	21	AAW33445	Human PR01155 prot
8	54.5	66	135	21	AAW66739	Membrane-bound pro
9	54.5	66	135	22	AAW65262	Human PR01155 (UNQ
10	49.5	49	51	20	AAW12634	Human 5' EST seque
11	22.3	27	39	20	AAW74414	HPMBQ91 protein se

85	6	5.0	127	21	AAB32666	Eucalyptus grandis	158	222	22	AAB61778	Sunflower pathogen
86	6	5.0	129	19	AAW69949	DN722_2 protein.	159	223	21	AAV44260	Asparagus officina
87	6	5.0	135	21	AAW59852	Autoantigen diagno	160	223	21	AAH61784	Sunflower pathogen
88	6	5.0	136	22	AAW65744	Rac2-related prote	161	224	21	AAV57749	Arabidopsis thalia
89	6	5.0	139	18	AAW23003	Canine herpesvirus	162	225	20	AAV59664	Secreted protein 1
90	6	5.0	139	19	AAW72663	Canine herpes viru	163	225	20	AAV42441	Cytokine family me
91	6	5.0	139	22	AAW51120	Canine herpes viru	164	225	20	AAW85731	z219a polypeptide
92	6	5.0	144	21	AAW59087	Breast and ovarian	165	225	20	AAV17835	Human PRO365 prote
93	6	5.0	145	19	AAW38463	Mouse RNA-binding	166	225	21	AAH25762	Human PRO365 polyp
94	6	5.0	146	21	AAW45988	Arabidopsis thalia	167	225	21	AAH01326	Human secreted pro
95	6	5.0	149	22	AAW99856	Physcomitrella pat	168	225	22	AAU12366	Human PRO365 polyp
96	6	5.0	153	20	AAW29391	Sperm whale myoglo	169	225	22	AAU14503	Human novel protei
97	6	5.0	153	20	AAW81769	Whale MYGL peptide	170	225	22	AAH85208	Human 2-21 protein
98	6	5.0	153	21	AAV69975	MYGL protein. Uni	171	225	22	AAE01045	Human secreted tum
99	6	5.0	154	21	AAW47234	Arabidopsis thalia	172	225	22	AAH31188	Amino acid sequenc
100	6	5.0	157	20	AAV31806	Beak and feather d	173	225	22	AAH75348	Secreted protein #
101	6	5.0	157	20	AAV81598	Streptococcus pneu	174	225	21	AAV79197	Human diarylsulfon
102	6	5.0	158	21	AAW47233	Arabidopsis thalia	175	225	20	AAH85732	z219a polypeptide
103	6	5.0	160	21	AAW53452	Arabidopsis thalia	176	225	20	AAH85732	Human polypeptide
104	6	5.0	161	21	AAW12312	Arabidopsis thalia	177	225	22	AAH41883	Escherichia coli F
105	6	5.0	161	22	AAW95034	Zea mays protein f	178	225	22	AAE03787	Human gene 1 encod
106	6	5.0	164	20	AAW03791	Human protein sequ	179	225	21	AAH03787	Arabidopsis thalia
107	6	5.0	166	21	AAW56356	S. aureus polytype	180	225	20	AAH57748	Human secreted tum
108	6	5.0	166	22	AAW18394	Human secreted pro	181	225	22	AAE01059	Human protein sequ
109	6	5.0	174	21	AAW41067	Peptide #4828 enco	182	225	20	AAH94584	Human secreted pro
110	6	5.0	175	18	AAW28333	Human ORFX ORF831	183	225	19	AAW72933	Myobacterium tube
111	6	5.0	175	21	AAW11131	Staphylococcus aur	184	225	20	AAV21953	Amino acid sequenc
112	6	5.0	175	21	AAW51901	Arabidopsis thalia	185	225	20	AAW56334	Homo sapiens secre
113	6	5.0	177	15	AAW60895	Borrelia J1 antige	186	225	22	AAW24121	Human EST encoded
114	6	5.0	177	15	AAW62781	Borrelia J1 antige	187	225	22	AAH38873	Human polypeptide
115	6	5.0	177	15	AAW62782	Borrelia J1 antige	188	225	22	AAH27243	Human polypeptide
116	6	5.0	177	17	AAW83037	Partial transposas	189	225	20	AAH29128	Amino acid sequenc
117	6	5.0	180	21	AAW28680	Arabidopsis thalia	190	225	20	AAV03752	S. aureus Ferrichr
118	6	5.0	183	20	AAV36865	Protein involved i	191	225	22	AAH82441	S. epidermidis ope
119	6	5.0	183	22	AAW65707	Novel protein kina	192	225	22	AAH71376	Human secreted pro
120	6	5.0	184	19	AAW38464	Mouse RNA-binding	193	225	22	AAW40659	Human polypeptide
121	6	5.0	187	21	AAW51842	Arabidopsis thalia	194	225	22	AAU01003	Human EXMAD-21 SEQ
122	6	5.0	187	22	AAU14267	Human novel protei	195	225	18	AAW37354	Amino acid sequenc
123	6	5.0	187	22	AAW91067	C glutamicum prote	196	225	21	AAV74966	Neisseria gonorrhoe
124	6	5.0	187	22	AAW80020	Corynebacterium gl	197	225	22	AAH90549	C glutamicum prote
125	6	5.0	190	21	AAW02786	Arabidopsis thalia	198	225	22	AAV49440	S. typhimurium ary
126	6	5.0	190	21	AAW09587	Arabidopsis thalia	199	225	21	AAH11686	A. vitis hypersens
127	6	5.0	190	21	AAW10859	Arabidopsis thalia	200	225	21	AAH44770	Soybean serine O-a
128	6	5.0	190	21	AAW37456	Arabidopsis thalia	201	225	20	AAW78467	Thermus species sp
129	6	5.0	191	21	AAW29836	Arabidopsis thalia	202	225	20	AAW78468	T. filiformis DNA p
130	6	5.0	193	22	AAW85210	21.5 kDa human 2-2	203	225	20	AAW78463	T. flavus DNA polym
131	6	5.0	194	15	AAW60896	Borrelia J1 antige	204	225	22	AAH91709	C glutamicum prote
132	6	5.0	196	21	AAW11130	Arabidopsis thalia	205	225	22	AAH78462	T. aquaticus DNA po
133	6	5.0	196	21	AAW51900	Arabidopsis thalia	206	225	21	AAH56653	Human prostate can
134	6	5.0	197	21	AAW07396	Arabidopsis thalia	207	225	21	AAH76748	Human protein kina
135	6	5.0	197	21	AAW30192	Arabidopsis thalia	208	225	22	AAE06206	Human protein kina
136	6	5.0	197	21	AAW32599	Arabidopsis thalia	209	225	22	AAH92549	C glutamicum prote
137	6	5.0	197	21	AAW48944	Arabidopsis thalia	210	225	22	AAH81198	Human RNA-binding
138	6	5.0	197	21	AAW33999	Arabidopsis thalia	211	225	22	AAH46733	T. aquaticus DNA p
139	6	5.0	198	21	AAW42941	Human ORFX ORF2705	212	225	300	AAH96265	Mutant Thermus aqu
140	6	5.0	199	21	AAW29835	Arabidopsis thalia	213	225	310	AAH96265	Arabidopsis thalia
141	6	5.0	199	21	AAW31741	Arabidopsis thalia	214	225	312	AAH96265	Arabidopsis thalia
142	6	5.0	200	21	AAW28679	Arabidopsis thalia	215	225	312	AAH93902	Amino acid sequenc
143	6	5.0	204	20	AAW34533	Porphomonas ging	216	225	314	AAH71117	Human Hydrolase pr
144	6	5.0	205	21	AAW48044	Arabidopsis thalia	217	225	315	AAH96268	Mutant Thermus aqu
145	6	5.0	206	22	AAW85209	22.8 kDa human 2-2	218	225	320	AAW24210	Cleavage BN/thromb
146	6	5.0	208	21	AAW51841	Arabidopsis thalia	219	225	320	AAW79955	Cleavage BN/thromb
147	6	5.0	208	21	AAV75093	Neisseria gonorrhoe	220	225	320	AAH59937	Amino acid sequenc
148	6	5.0	208	21	AAW75094	Neisseria meningit	221	225	322	AAH96266	Thermus aquaticus
149	6	5.0	211	22	AAW62722	B. garinii ospC pro	222	225	322	AAH72129	Human olfactory re
150	6	5.0	212	12	AAH13140	B. burgdorferi stra	223	225	323	AAH72532	Human OR-like poly
151	6	5.0	212	16	AAW75729	B. burgdorferi str	224	225	323	AAH93767	Human protein sequ
152	6	5.0	212	18	AAW41824	B. afzeiili Ospc.	225	225	325	AAH95335	Human quaking spll
153	6	5.0	212	22	AAW40188	Human polypeptide	226	225	325	AAH95335	C glutamicum prote
154	6	5.0	219	21	AAW07285	Arabidopsis thalia	227	225	327	AAH96086	Human gene 46 enco
155	6	5.0	219	21	AAW09586	Arabidopsis thalia	228	225	328	AAH08544	Mesothelin related
156	6	5.0	219	21	AAW37455	Arabidopsis thalia	229	225	328	AAH87109	Human secreted pro
157	6	5.0	221	20	AAW34400	Porphomonas ging	230	225	329	AAH36232	Arabidopsis thalia

231	6	5.0	330	22	AAG92260	C glutamicum prote	304	459	19	AAW38457	Human RNA-binding
232	6	5.0	332	22	AAG20055	C glutamicum prote	305	463	22	AAW71254	Human gene 12-enco
233	6	5.0	333	22	AAW42076	Human polypeptide	306	465	21	AAW83150	NGSP polypeptide o
234	6	5.0	337	21	AAW12503	Human MATH-2 prote	307	467	22	AAW88483	Human membrane or
235	6	5.0	337	22	AAW60352	Mouse atonal homol	308	470	22	AAW40522	Human polypeptide
236	6	5.0	337	22	AAW60368	Mouse atonal homol	309	470	22	AAW40522	Human polypeptide
237	6	5.0	341	21	AAW95336	Human quaking spli	310	475	21	AAW70414	Neisseria meningit
238	6	5.0	342	20	AAW07862	Human secreted pro	311	478	22	AAW20314	Soybean apoptosis
239	6	5.0	344	17	AAW40918	Human quaking spli	312	482	18	AAW06540	C5a-like seven tra
240	6	5.0	348	14	AAW01619	Bacillus subtilis	313	483	19	AAW37064	HIV-1 breakthrough
241	6	5.0	348	21	AAW54118	Human uridine diph	314	483	21	AAW18325	Arabidopsis thalia
242	6	5.0	354	21	AAW51152	Amino acid sequenc	315	483	21	AAW46788	Arabidopsis thalia
243	6	5.0	354	21	AAW36231	Human UDP galactos	316	484	8	AAW70458	Sequence of gpD en
244	6	5.0	356	22	AAW92897	Arabidopsis thalia	317	486	22	AAW33541	Human protein sequ
245	6	5.0	358	21	AAW04826	C glutamicum prote	318	487	19	AAW37065	HIV-1 breakthrough
246	6	5.0	358	21	AAW61479	Arabidopsis thalia	319	489	22	AAW71293	Human gene 12-enco
247	6	5.0	363	22	AAW03764	Arabidopsis thalia	320	491	16	AAW72369	Human auxillary cy
248	6	5.0	368	22	AAW76567	Human gene 1 encod	321	491	17	AAW93176	Human cytochrome p
249	6	5.0	370	21	AAW52996	Corynebacterium g1	322	491	17	AAW81468	Human derived cyto
250	6	5.0	371	20	AAW95171	Neisseria meningit	323	498	21	AAW70413	Neisseria meningit
251	6	5.0	374	13	AAW25049	Protein exhibiting	324	499	21	AAW75748	Neisseria gonorrh
252	6	5.0	375	19	AAW98466	H. pylori GHPO 782	325	499	21	AAW75749	Neisseria meningit
253	6	5.0	376	21	AAW36230	Human cytochrome P	326	499	21	AAW75750	Neisseria meningit
254	6	5.0	377	19	AAW70902	Corynebacterium g1	327	499	21	AAW52993	Neisseria meningit
255	6	5.0	380	22	AAW80034	Human secreted pro	328	499	21	AAW52994	Neisseria meningit
256	6	5.0	381	20	AAW81821	Human ZIRI protein	329	499	21	AAW52995	Neisseria meningit
257	6	5.0	381	20	AAW55787	Human zinc RING (2	330	502	21	AAW53884	Neisseria meningit
258	6	5.0	386	22	AAW62727	Borrelia sp chimer	331	504	21	AAW16593	Arabidopsis thalia
259	6	5.0	390	20	AAW42325	Human TOSO protein	332	511	9	AAW81161	Arabidopsis thalia
260	6	5.0	390	20	AAW17496	Human TOSO protein	333	511	9	AAW81180	Recombinant alpha-
261	6	5.0	392	21	AAW05001	Human PIGRL-1 prot	334	512	11	AAW07574	Sequence of alpha-
262	6	5.0	393	21	AAW54097	Human PIGRL-1 prot	335	512	11	AAW07574	Alpha-amyase enco
263	6	5.0	402	21	AAW08543	Human pancreatic c	336	515	15	AAW48670	Chitinase derivati
264	6	5.0	402	21	AAW77276	Mesothelin related	337	516	16	AAW80279	N. crassa cellobio
265	6	5.0	402	21	AAW08547	Soluble mesothelin	338	517	22	AAW74679	Human protease and
266	6	5.0	402	21	AAW77276	Streptomyces cinna	339	528	17	AAW96267	Mutant Thermus aqu
267	6	5.0	402	21	AAW77276	Amino acid sequenc	340	532	21	AAW22283	Arabidopsis thalia
268	6	5.0	402	21	AAW78828	Human secreted pro	341	532	21	AAW39876	Arabidopsis thalia
269	6	5.0	403	21	AAW42261	Human gene 46 enco	342	541	19	AAW77406	Arabidopsis thalia
270	6	5.0	404	21	AAW8196	Borrelia sp chimer	343	541	19	AAW77406	Arabidopsis thalia
271	6	5.0	404	21	AAW8196	Arabidopsis thalia	344	547	21	AAW39875	Heat shock protein
272	6	5.0	410	22	AAW62740	Arabidopsis thalia	345	547	22	AAW69060	Arabidopsis thalia
273	6	5.0	414	21	AAW04825	Arabidopsis thalia	346	548	17	AAW96263	Pseudomonas aerugi
274	6	5.0	414	21	AAW53885	Arabidopsis thalia	347	548	17	AAW96263	Mutant Thermus aqu
275	6	5.0	414	21	AAW61478	Arabidopsis thalia	348	549	21	AAW14497	Arabidopsis thalia
276	6	5.0	414	21	AAW83151	NGSP polypeptide o	349	551	20	AAW23907	Arabidopsis thalia
277	6	5.0	415	21	AAW04824	Arabidopsis thalia	350	551	20	AAW23907	Amino acid sequenc
278	6	5.0	415	21	AAW04824	Arabidopsis thalia	351	553	21	AAW97004	S. cerevisiae esse
279	6	5.0	415	21	AAW04824	Arabidopsis thalia	352	557	16	AAW79586	Mouse TCP-1 subuni
280	6	5.0	429	20	AAW16594	Human cytochrome P	353	557	21	AAW53140	Macaca mulatta rha
281	6	5.0	429	21	AAW80086	Citrate transport	354	560	22	AAW33403	Arabidopsis thalia
282	6	5.0	430	21	AAW22042	Arabidopsis thalia	355	560	22	AAW62724	Borrelia sp chimer
283	6	5.0	431	20	AAW42295	Human cytochrome P	356	563	19	AAW56476	Amino acid sequenc
284	6	5.0	439	18	AAW23447	Pseudomonas putida	357	564	22	AAW62100	Human bridging int
285	6	5.0	439	18	AAW23447	Pseudomonas putida	358	565	21	AAW70011	Human protease and
286	6	5.0	439	18	AAW23450	Pseudomonas putida	359	565	21	AAW32435	Human ubiquitin sp
287	6	5.0	439	18	AAW23453	Pseudomonas putida	360	570	21	AAW94912	Human chaperone pr
288	6	5.0	439	18	AAW23454	Pseudomonas putida	361	570	21	AAW94912	Human secreted pro
289	6	5.0	439	19	AAW38466	Mouse RNA-binding	362	574	22	AAW69061	pTcHisB expressio
290	6	5.0	441	21	AAW14499	Arabidopsis thalia	363	576	16	AAW1375	Rat GRK encoded by
291	6	5.0	441	21	AAW22041	Arabidopsis thalia	364	576	16	AAW1374	Human GRK #2. Hom
292	6	5.0	442	18	AAW23448	Pseudomonas putida	365	576	20	AAW23925	Amino acid sequenc
293	6	5.0	442	18	AAW23456	Pseudomonas putida	366	576	22	AAW84262	HTM clone 1253545
294	6	5.0	444	18	AAW23456	Pseudomonas putida	367	579	22	AAW84527	Amino acid sequenc
295	6	5.0	448	21	AAW70409	Neisseria meningit	368	581	22	AAW59832	Human protein sequ
296	6	5.0	449	21	AAW43854	Human cancer assoc	369	594	21	AAW16592	TutI protein. Tha
297	6	5.0	452	18	AAW23452	Pseudomonas putida	370	594	21	AAW53883	Arabidopsis thalia
298	6	5.0	453	21	AAW43841	Human cancer assoc	371	601	21	AAW79240	Arabidopsis thalia
299	6	5.0	454	20	AAW06921	Human ZIP-kinase (372	609	20	AAW37619	Human diarylsulfon
300	6	5.0	454	22	AAW94378	Human protein sequ	373	611	22	AAW85021	Amino acid sequenc
301	6	5.0	455	22	AAW68328	Amino acid sequenc	374	622	15	AAW53992	Shrimp white spot
302	6	5.0	459	18	AAW23451	Pseudomonas putida	375	622	15	AAW53992	Megakaryocyte pote
303	6	5.0	459	19	AAW38454	Mouse RNA-binding	376	632	18	AAW26674	Human CAK1 antigen
								633	21	AAW13373	Human GRK #1. Hom
										AAW31402	Arabidopsis thalia

377	6	5.0	650	21	AAB42495	Human ORFX ORF2259	450	6	5.0	888	22	AAW40290	Human polypeptide
378	6	5.0	654	22	AAB95459	Human protein sequ	451	6	5.0	889	20	AAW24913	Human ontherin. H
379	6	5.0	672	22	AAB93091	Human protein sequ	452	6	5.0	889	20	AAW21687	Cadherin-like poly
380	6	5.0	686	21	AAG31401	Arabidopsis thalia	453	6	5.0	908	20	AAW33450	Chimeric taq DNA p
381	6	5.0	695	17	AAR96264	Mutant Thermus aqu	454	6	5.0	908	20	AAW33451	Chimeric taq DNA p
382	6	5.0	720	22	AAW72081	Nicotiana tabacum	455	6	5.0	910	20	AAW33448	Chimeric taq DNA p
383	6	5.0	737	16	AAR76640	Deltex protein. H	456	6	5.0	910	20	AAW33449	Chimeric taq DNA p
384	6	5.0	737	16	AAR76639	Deltex protein pro	457	6	5.0	931	16	AAW79009	Human RNA repair p
385	6	5.0	737	18	AAW18317	Drosophila Deltex	458	6	5.0	941	22	AAW04778	Human vesicle traf
386	6	5.0	738	22	AAW32927	Human polypeptide	459	6	5.0	948	17	AAW53332	Tumor necrosis fac
387	6	5.0	745	22	AAW41083	Human polypeptide	460	6	5.0	948	18	AAW35375	TNF-R1-DD ligand p
388	6	5.0	748	22	AAW40225	Human polypeptide	461	6	5.0	949	20	AAW33452	Chimeric taq DNA p
389	6	5.0	757	13	AAW23141	Mutant thermostabl	462	6	5.0	982	20	AAW33453	Chimeric taq DNA p
390	6	5.0	758	13	AAW23154	Mutant thermostabl	463	6	5.0	1029	21	AAW24027	Human PRO3434 prot
391	6	5.0	783	21	AAW75533	Neisseria meningit	464	6	5.0	1029	21	AAW96736	PRO3434, a novel s
392	6	5.0	783	21	AAW75534	Neisseria meningit	465	6	5.0	1054	22	AAW68897	Human HX2004-6 pro
393	6	5.0	787	13	AAW23142	Mutant thermostabl	466	6	5.0	1054	22	AAW68898	Human HX2004-6 pro
394	6	5.0	788	13	AAW23153	Mutant thermostabl	467	6	5.0	1077	22	AAW01924	Human adenylyase cy
395	6	5.0	797	21	AAB40601	Human ORFX ORF365	468	6	5.0	1141	22	AAW85008	Shrimp white spot
396	6	5.0	810	22	AAB62314	T. aquaticus (Taq)	469	6	5.0	1156	21	AAW10104	Feline foamy virus
397	6	5.0	823	17	AAW00364	Human CDC27. Homo	470	6	5.0	1221	20	AAW05940	Thermophilus therm
398	6	5.0	823	19	AAW98507	H. pylori GHPO 122	471	6	5.0	1255	20	AAW05944	Thermophilus therm
399	6	5.0	824	16	AAW75848	H-NOC retinoblasto	472	6	5.0	1272	21	AAW70596	Rat multidrug resi
400	6	5.0	830	13	AAW23152	Mutant thermostabl	473	6	5.0	1272	21	AAW70597	Rat multidrug resi
401	6	5.0	830	16	AAR76060	Tfifl DNA-polymeras	474	6	5.0	1275	21	AAW78879	Rat mdrlb2 multidr
402	6	5.0	831	16	AAR64273	T. flavus DNA-poly	475	6	5.0	1275	22	AAW60409	P. chrysogenum ABC
403	6	5.0	831	19	AAW79961	Thermus flavus DNA	476	6	5.0	1297	22	AAW62491	Human protein sequ
404	6	5.0	831	20	AAW80428	DNA polymerase enz	477	6	5.0	1504	21	AAW95729	Murine APC-2 polyp
405	6	5.0	832	10	AAW90556	Purified native th	478	6	5.0	1674	21	AAW92060	Novel protein kin
406	6	5.0	832	13	AAW23140	Mutant thermostabl	479	6	5.0	1920	22	AAW65856	Novel APC-2 protei
407	6	5.0	832	13	AAW22602	Taq polymerase enc	480	6	5.0	2274	22	AAW50674	Mouse APC-2 protei
408	6	5.0	832	13	AAW22603	Taq polymerase enc	481	6	5.0	2473	17	AAW97244	Virulence gene clu
409	6	5.0	832	13	AAW22604	Taq polymerase enc	482	6	5.0	7257	21	AAW58576	Sorangium cellulos
410	6	5.0	832	16	AAW76690	Taq DNA-polymerase	483	6	5.0	4473	16	AAW87912	Peptide antagonisi
411	6	5.0	832	16	AAW76691	DNA-polymerase REM	484	6	5.0	4473	16	AAW87912	Peptide antagonisi
412	6	5.0	832	16	AAW76692	DNA-polymerase REM	485	6	5.0	4473	16	AAW87912	Hepatitis C virus
413	6	5.0	832	16	AAW76693	DNA-polymerase (F7	486	6	5.0	4473	16	AAW87912	Hepatitis C virus
414	6	5.0	832	16	AAW64272	T. aquaticus DNA-p	487	6	5.0	4473	16	AAW87912	Peptide encoded by
415	6	5.0	832	19	AAW79960	Thermus aquaticus	488	6	5.0	4473	16	AAW87912	Peptide encoded by
416	6	5.0	832	19	AAW79963	Thermus DNA polym	489	6	5.0	4473	16	AAW87912	Amino acid probe f
417	6	5.0	832	19	AAW76209	T. aquaticus DNA p	490	6	5.0	4473	16	AAW87912	B. thuringiensis e
418	6	5.0	832	19	AAW76210	T. aquaticus DNA p	491	6	5.0	4473	16	AAW87912	Tumour homing pep
419	6	5.0	832	19	AAW76211	T. aquaticus DNA p	492	6	5.0	4473	16	AAW87912	Human breast cance
420	6	5.0	832	19	AAW76208	T. aquaticus DNA p	493	6	5.0	4473	16	AAW87912	Human breast tumou
421	6	5.0	832	19	AAW76203	T. aquaticus DNA p	494	6	5.0	4473	16	AAW87912	Peptide #2 used in
422	6	5.0	832	19	AAW76204	T. aquaticus DNA p	495	6	5.0	4473	16	AAW87912	Peptide probe #2.
423	6	5.0	832	19	AAW76205	T. aquaticus DNA p	496	6	5.0	4473	16	AAW87912	HBV pol 541 peptid
424	6	5.0	832	19	AAW76206	T. aquaticus DNA p	497	6	5.0	4473	16	AAW87912	Alternative ORF3 e
425	6	5.0	832	19	AAW76207	T. aquaticus DNA p	498	6	5.0	4473	16	AAW87912	Hepatitis B virus
426	6	5.0	832	19	AAW61087	Taq DNA polymerase	499	6	5.0	4473	16	AAW87912	Tumour antigen pep
427	6	5.0	832	19	AAW61088	Taq DNA polymerase	500	6	5.0	4473	16	AAW87912	Peptide fragment o
428	6	5.0	832	19	AAW61089	Taq DNA polymerase	501	6	5.0	4473	16	AAW87912	Fragment of nemato
429	6	5.0	832	19	AAW61090	Taq DNA polymerase	502	6	5.0	4473	16	AAW87912	LXXLL signature mo
430	6	5.0	832	19	AAW61091	Taq DNA polymerase	503	6	5.0	4473	16	AAW87912	Human complementa
431	6	5.0	832	19	AAW61092	Taq DNA polymerase	504	6	5.0	4473	16	AAW87912	Human complementa
432	6	5.0	832	19	AAW23962	Modified taq polym	505	6	5.0	4473	16	AAW87912	Human complementa
433	6	5.0	832	19	AAW80427	DNA polymerase enz	506	6	5.0	4473	16	AAW87912	Human complementa
434	6	5.0	832	22	AAW67547	Amino acid sequenc	507	6	5.0	4473	16	AAW87912	Human complementa
435	6	5.0	832	22	AAW67549	Amino acid sequenc	508	6	5.0	4473	16	AAW87912	Human complementa
436	6	5.0	833	16	AAW64275	DNA-polymerase con	509	6	5.0	4473	16	AAW87912	Human complementa
437	6	5.0	833	17	AAW96262	Mutant Thermus aqu	510	6	5.0	4473	16	AAW87912	Human complementa
438	6	5.0	833	18	AAW24211	Cleavage DN nuclea	511	6	5.0	4473	16	AAW87912	Human complementa
439	6	5.0	833	18	AAW24212	Cleavage DA nuclea	512	6	5.0	4473	16	AAW87912	Human complementa
440	6	5.0	833	18	AAW24213	Cleavage DV nuclea	513	6	5.0	4473	16	AAW87912	Human complementa
441	6	5.0	833	19	AAW79966	Cleavage DV nuclea	514	6	5.0	4473	16	AAW87912	Human complementa
442	6	5.0	833	19	AAW79967	Cleavage DV nuclea	515	6	5.0	4473	16	AAW87912	Human complementa
443	6	5.0	833	19	AAW79968	Cleavage DV nuclea	516	6	5.0	4473	16	AAW87912	Human complementa
444	6	5.0	833	19	AAW59941	Amino acid sequenc	517	6	5.0	4473	16	AAW87912	Human complementa
445	6	5.0	833	19	AAW59938	Amino acid sequenc	518	6	5.0	4473	16	AAW87912	Human complementa
446	6	5.0	833	19	AAW59942	Amino acid sequenc	519	6	5.0	4473	16	AAW87912	Human complementa
447	6	5.0	833	20	AAW80430	Consensus sequence	520	6	5.0	4473	16	AAW87912	Human complementa
448	6	5.0	845	16	AAW72875	Tsps17 polymerase.	521	6	5.0	4473	16	AAW87912	Human complementa
449	6	5.0	851	22	AAW72617	Carassius auratus	522	6	5.0	4473	16	AAW87912	Human complementa

523	10	22	AAG844008	Arabidopsis thalia	596	4.1	21	14	AAR45053	Basic (positively
524	10	22	AG844261	Arabidopsis thalia	597	4.1	21	14	AAR45054	Basic (positively
525	10	22	AG844262	Arabidopsis thalia	598	4.1	21	14	AAR36312	Amphiphilic ion ch
526	10	22	AG844263	Arabidopsis thalia	599	4.1	21	14	AAR36313	Amphiphilic ion ch
527	10	22	AG844264	Arabidopsis thalia	600	4.1	21	14	AAR31083	C-terminal substd.
528	10	22	AG844265	Arabidopsis thalia	601	4.1	21	14	AAR31084	C-terminal substd.
529	11	9	AAP82891	N-terminal of hg-C	602	4.1	21	14	AAR31084	C-terminal substd.
530	11	11	AAR11923	B. burgdorferi pc-	603	4.1	21	14	AAR35301	Amphiphilic peptid
531	11	12	AAR12103	B. burgdorferi pc-	604	4.1	21	14	AAR35302	Amphiphilic peptid
532	11	20	AAV31131	B. burgdorferi pc-	605	4.1	21	14	AAR39015	Biologically activ
533	11	20	AAW67678	B. burgdorferi pc-	606	4.1	21	14	AAR39016	Biologically activ
534	11	21	AAW88539	LXIII signature mo	607	4.1	21	15	AAR55907	Ion channel formin
535	11	21	AAW88539	NCAM Igl binding p	608	4.1	21	15	AAR55908	Ion channel formin
536	11	22	AAW86343	G. suboxydans DSM	609	4.1	21	15	AAR50483	Amphiphilic pepti
537	12	19	AAW80588	Peptide fragment f	610	4.1	21	15	AAR50484	Amphiphilic peptid
538	12	22	AAW67000	Fl-scd2K peptide.	611	4.1	21	15	AAR50367	Amphiphilic peptid
539	13	7	AAP61493	Sequence of LbH-C4	612	4.1	21	15	AAR50368	Amphiphilic pepti
540	13	13	AAR98232	Tau protein phosph	613	4.1	21	15	AAR50368	Amphiphilic pepti
541	13	21	AAW21965	Phosphorylated tau	614	4.1	21	15	AAR50368	Amphiphilic pepti
542	14	10	AAP97794	Sequence of fragme	615	4.1	21	15	AAR50368	Amphiphilic pepti
543	14	14	AAR32977	Mastoparan analogu	616	4.1	21	15	AAR50368	Amphiphilic pepti
544	14	14	AAR32983	Mastoparan analogu	617	4.1	21	15	AAR50368	Amphiphilic pepti
545	14	16	AAR70461	VH sequence of ant	618	4.1	21	16	AAR90076	Peptide which neut
546	15	12	AAW14809	ves oncogene prote	619	4.1	21	16	AAR90076	Peptide which neut
547	15	12	AAR13979	[Leu12,Lys14]Melit	620	4.1	21	16	AAR83847	Cancer treating, a
548	15	16	AAW61470	[Leu12,Lys14]Melit	621	4.1	21	16	AAR83847	(KALSKAL)3 peptid
549	15	19	AAW20842	Human neurofilamen	622	4.1	21	20	AAV10671	(KLKALG)3 peptid
550	15	21	AAW07617	A human alpha-heli	623	4.1	21	20	AAV10671	Ion channel formin
551	15	21	AAW93013	Transforming growt	624	4.1	21	20	AAV10671	Peptide used to ma
552	15	21	AAW03303	Human epitope Rb50	625	4.1	21	20	AAV10671	Peptide used to ma
553	15	21	AAW52604	v-fes encoded onco	626	4.1	21	20	AAV10671	Peptide used to ma
554	15	21	AAW52671	v-fes encoded onco	627	4.1	21	20	AAV10671	Peptide used to ma
555	15	22	AAU00751	Human HTAU40 (R2-R	628	4.1	21	20	AAV10671	Peptide used to ma
556	15	22	AAU00752	Human HTAU40 (R2-R	629	4.1	21	20	AAV10671	Peptide used to ma
557	15	22	AAU00753	Human HTAU40 (R2-R	630	4.1	21	20	AAV10671	Peptide used to ma
558	16	17	AAW04534	HPC heavy chain N-	631	4.1	21	20	AAV10671	Peptide used to ma
559	16	17	AAW04534	HPC heavy chain N-	632	4.1	21	20	AAV10671	Peptide used to ma
560	17	17	AAW04532	HPC transgenic mou	633	4.1	21	20	AAV10671	Peptide used to ma
561	17	17	AAW98230	Tau protein phosph	634	4.1	21	20	AAV10671	Peptide used to ma
562	17	20	AAW56642	Secreted protein e	635	4.1	21	20	AAV10671	Peptide used to ma
563	17	20	AAW25450	Human secreted pro	636	4.1	21	20	AAV10671	Peptide used to ma
564	17	20	AAW35881	Signal peptide of	637	4.1	21	20	AAV10671	Peptide used to ma
565	17	20	AAW12669	Human 5' EST secre	638	4.1	21	20	AAV10671	Peptide used to ma
566	17	20	AAW11368	Human 5' EST secre	639	4.1	21	20	AAV10671	Peptide used to ma
567	17	20	AAW11710	Peptide encoded by	640	4.1	21	20	AAV10671	Peptide used to ma
568	17	20	AAW12515	Human 5' EST signa	641	4.1	21	20	AAV10671	Peptide used to ma
569	17	20	AAW04165	Human secreted pro	642	4.1	21	20	AAV10671	Peptide used to ma
570	17	20	AAW04147	Human secreted pro	643	4.1	21	20	AAV10671	Peptide used to ma
571	17	21	AAW00013	Human secreted pro	644	4.1	21	20	AAV10671	Peptide used to ma
572	17	22	AAW04088	Human 48-19-3-GI-F	645	4.1	21	20	AAV10671	Peptide used to ma
573	18	14	AAW54456	Signal peptide enc	646	4.1	21	20	AAV10671	Peptide used to ma
574	18	14	AAW54456	Disclosed Amb a 1.	647	4.1	21	20	AAV10671	Peptide used to ma
575	18	15	AAW47084	Systemin. lycoper	648	4.1	21	20	AAV10671	Peptide used to ma
576	18	18	AAW35734	Eukaryotic folding	649	4.1	21	20	AAV10671	Peptide used to ma
577	18	19	AAW62033	Sequence of the ju	650	4.1	21	20	AAV10671	Peptide used to ma
578	18	19	AAW62033	PD3 specific pept	651	4.1	21	20	AAV10671	Peptide used to ma
579	18	20	AAW99102	Tomato systemin.	652	4.1	21	20	AAV10671	Peptide used to ma
580	18	20	AAW97629	Tomato peptide hor	653	4.1	21	20	AAV10671	Peptide used to ma
581	18	20	AAW97630	Systemin-like pept	654	4.1	21	20	AAV10671	Peptide used to ma
582	18	21	AAW97631	Systemin-like pept	655	4.1	21	20	AAV10671	Peptide used to ma
583	18	21	AAW30686	Amino acid sequenc	656	4.1	21	20	AAV10671	Peptide used to ma
584	18	21	AAW30687	Amino acid sequenc	657	4.1	21	20	AAV10671	Peptide used to ma
585	18	21	AAW30688	Amino acid sequenc	658	4.1	21	20	AAV10671	Peptide used to ma
586	18	22	AAW92381	Miscellaneous pept	659	4.1	21	20	AAV10671	Peptide used to ma
587	20	15	AAW89867	Cancer treating, a	660	4.1	21	20	AAV10671	Peptide used to ma
588	20	16	AAW13196	Fragment of p53 bi	661	4.1	21	20	AAV10671	Peptide used to ma
589	20	19	AAW69447	HCG antigenic pept	662	4.1	21	20	AAV10671	Peptide used to ma
590	20	19	AAW57347	Human Wbpl immunog	663	4.1	21	20	AAV10671	Peptide used to ma
591	20	20	AAW933468	Synthetic antigeni	664	4.1	21	20	AAV10671	Peptide used to ma
592	20	21	AAW90974	Synthetic antigeni	665	4.1	21	20	AAV10671	Peptide used to ma
593	20	21	AAW51391	Human periplasmic	666	4.1	21	20	AAV10671	Peptide used to ma
594	20	21	AAW50993	Human S182 5'-UTR	667	4.1	21	20	AAV10671	Peptide used to ma
595	20	22	AAU02874	Potato pr17-WT pro	668	4.1	21	20	AAV10671	Peptide used to ma
	20	22	AAU01177	Human Chorionic Go						
	20	22	AAU01177	Synthetic human ch						

Basic (positively)
Basic (positively)
Amphiphilic ion ch
Amphiphilic ion ch
C-terminal substd.
C-terminal substd.
Amphiphilic peptid
Amphiphilic peptid
Biologically activ
Biologically activ
Ion channel formin
Ion channel formin
Amphiphilic pepti
Amphiphilic pepti
Amphiphilic peptid
Amphiphilic peptid
Peptide which neut
Peptide which neut
Cancer treating, a
(KALSKAL)3 peptid
(KLKALG)3 peptid
Ion channel formin
Ion channel formin
Peptide used to ma
Peptide used to ma
Lecithin:cholester
Lecithin:cholester
Lecithin:cholester
Lecithin:cholester
Lecithin:cholester
Lecithin:cholester
Lecithin:cholester
Lecithin:cholester
Lecithin:cholester
Lecithin:cholester
Peptide encoded by
Human TAU derived
Bcl-2 related prot
Human secreted pro
Tachykinins peptid
LW5-HL BH2 domain
Part of elastomer
PR-R major fragmen
PR-R major fragmen
Peptide #9834 enco
ATP-binding casset
Tachykinins peptid
Laccase internal p
Secreted protein e
Farnesoid X recept
Human nuclear rece
Peptide #3217 enco
Peptide #3305 enco
Peptide #3182 enco
Herpes simplex vir
Human secreted pro
PR-R minor fragmen
PR-R minor amino a
Human TAU derived
HCG antigenic pept
Synthetic antigeni
Peptide #6763 enco
Peptide #6658 enco
Synthetic HCG anti
Human chorionic go
SEQ ID NO 443 from
Peptide for Tn ant
Human secreted pro
Human secreted pro
Peptide from the 3

669	4.1	29	20	AAW83091	Peptide from the 3	742	5	4.1	43	21	AAW94692	Human zslg93 epit
670	4.1	30	5	AAW40384	Sequence of synthe	743	5	4.1	43	22	AAW15008	Peptide #1442 enco
671	4.1	30	12	AAW14803	fes oncogene prote	744	5	4.1	43	22	AAW17615	Peptide #14049 enco
672	4.1	30	20	AAW36687	Fragment of human	745	5	4.1	43	22	AAW27445	Peptide #1482 enco
673	4.1	30	20	AAW25325	Human pancreatic p	746	5	4.1	43	22	AAW30133	Peptide #1470 enco
674	4.1	30	20	AAW12930	Amino acid sequenc	747	5	4.1	43	22	AAW02736	Peptide #1418 enco
675	4.1	30	20	AAW83090	Peptide from the 3	748	5	4.1	43	22	AAW05274	Peptide #3956 enco
676	4.1	30	21	AAW52601	v-fes encoded onco	749	5	4.1	43	22	AAW77787	Human colon cancer
677	4.1	30	22	AAW00775	Human TAU derived	750	5	4.1	44	22	AAW34270	Peptide #8307 enco
678	4.1	31	22	AAW55106	Tau protein fragme	751	5	4.1	45	18	AAW20450	H. pylori secreted
679	4.1	32	12	AAW12834	HIV protecting vac	752	5	4.1	45	20	AAW27663	Human secreted pro
680	4.1	32	20	AAW26637	SV4-derived lipope	753	5	4.1	45	20	AAW12762	Human 5' EST secre
681	4.1	32	21	AAW33995	Human secreted pro	754	5	4.1	45	21	AAW57037	Arabidopsis thalia
682	4.1	32	21	AAW44627	Human secreted pro	755	5	4.1	46	21	AAW37356	Human secreted pro
683	4.1	32	22	AAW61947	Modified [Ala17]H	756	5	4.1	46	22	AAW31704	Peptide #5741 enco
684	4.1	33	21	AAW09315	Hepatitis GB virus	757	5	4.1	46	22	AAW76321	Human colon cancer
685	4.1	33	21	AAW58301	Human p160 coactiv	758	5	4.1	47	20	AAW13000	Human secreted pro
686	4.1	33	21	AAW64883	Human 5' EST relat	759	5	4.1	47	21	AAW07623	A human alpha-hell
687	4.1	34	21	AAW32440	Human secreted pro	760	5	4.1	47	21	AAW07642	Amino acid sequenc
688	4.1	35	10	AAW91352	Amino acid sequenc	761	5	4.1	48	20	AAW02923	Fragment of human
689	4.1	35	10	AAW94257	S protein from lam	762	5	4.1	48	21	AAW27581	Human secreted pro
690	4.1	35	19	AAW75127	Human secreted pro	763	5	4.1	48	21	AAW18419	Peptide #4853 enco
691	4.1	35	20	AAW08477	Human BS274 protei	764	5	4.1	48	22	AAW21905	Peptide #8339 enco
692	4.1	35	21	AAW45087	Human secreted pro	765	5	4.1	48	22	AAW30896	Peptide #4933 enco
693	4.1	35	21	AAW33148	Human secreted pro	766	5	4.1	48	22	AAW38233	Peptide #12270 enco
694	4.1	35	21	AAW33148	Eucalyptus grandis	767	5	4.1	48	22	AAW06018	Peptide #4700 enco
695	4.1	35	22	AAW35322	Peptide #9359 enco	768	5	4.1	49	8	AAW70036	Secretory signal s
696	4.1	36	10	AAW91353	Amino acid sequenc	769	5	4.1	49	22	AAW23855	Human EST encoded
697	4.1	36	22	AAW16655	Peptide #3089 enco	770	5	4.1	49	22	AAW91783	C glutamicum prote
698	4.1	36	22	AAW29139	Peptide #3176 enco	771	5	4.1	49	22	AAW31651	Amino acid sequenc
699	4.1	36	22	AAW04371	Peptide #3053 enco	772	5	4.1	50	21	AAW56577	Arabidopsis thalia
700	4.1	36	22	AAW77762	Human colon cancer	773	5	4.1	50	21	AAW06603	Human foetal prote
701	4.1	37	13	AAW29218	Thr(13)His(21)Leu(774	5	4.1	51	21	AAW55275	Arabidopsis thalia
702	4.1	37	13	AAW29218	Thr(13)Arg(18)His(775	5	4.1	51	21	AAW55275	Arabidopsis thalia
703	4.1	37	14	AAW38822	Thr13, His21, Leu2	776	5	4.1	51	21	AAW61663	Arabidopsis thalia
704	4.1	37	14	AAW38824	Thr13, Arg18, His2	777	5	4.1	51	21	AAW30271	Human secreted pro
705	4.1	37	19	AAW74603	Amino acid sequenc	778	5	4.1	51	22	AAW73742	Chaperone cpn60 pr
706	4.1	37	19	AAW74604	Amino acid sequenc	779	5	4.1	52	21	AAW44032	Human cancer assoc
707	4.1	37	20	AAW22455	Thr13, His21, Leu2	780	5	4.1	52	21	AAW66029	Telomerase associa
708	4.1	37	20	AAW22457	Human amylin agoni	781	5	4.1	52	22	AAW18899	Peptide #5333 enco
709	4.1	37	20	AAW90160	Human amylin agoni	782	5	4.1	52	22	AAW31438	Peptide #5475 enco
710	4.1	37	20	AAW90162	Human amylin agoni	783	5	4.1	53	21	AAW56576	Arabidopsis thalia
711	4.1	37	20	AAW88882	Polypeptide fragme	784	5	4.1	53	21	AAW06421	Human foetal prote
712	4.1	37	21	AAW44787	Human secreted pro	785	5	4.1	54	17	AAW01176	Serine protease pf
713	4.1	37	21	AAW45344	Human secreted pro	786	5	4.1	54	20	AAW27827	Human secreted pro
714	4.1	37	21	AAW18595	Amino acid sequenc	787	5	4.1	54	21	AAW57910	Arabidopsis thalia
715	4.1	37	21	AAW18597	Amino acid sequenc	788	5	4.1	54	21	AAW61712	Arabidopsis thalia
716	4.1	38	15	AAW54065	Non-A, non-B hepat	789	5	4.1	54	22	AAW14086	Peptide #520 enco
717	4.1	38	21	AAW36559	Arabidopsis thalia	790	5	4.1	54	22	AAW17999	Peptide #4433 enco
718	4.1	38	22	AAW20610	Peptide #7044 enco	791	5	4.1	54	22	AAW26493	Peptide #530 enco
719	4.1	38	22	AAW31361	Peptide #5398 enco	792	5	4.1	54	22	AAW30510	Peptide #4547 enco
720	4.1	38	22	AAW35598	Peptide #9635 enco	793	5	4.1	54	22	AAW36572	Peptide #10609 enco
721	4.1	38	22	AAW36701	Peptide #10738 enc	794	5	4.1	54	22	AAW01826	Peptide #508 enco
722	4.1	38	22	AAW76624	Human colon cancer	795	5	4.1	54	22	AAW05640	Peptide #4322 enco
723	4.1	38	22	AAW31646	Amino acid sequenc	796	5	4.1	54	22	AAW76999	Human colon cancer
724	4.1	39	21	AAW13631	Arabidopsis thalia	797	5	4.1	54	22	AAW50572	Flea serine protea
725	4.1	39	22	AAW01053	Human secreted pro	798	5	4.1	55	20	AAW36294	Human secreted pro
726	4.1	40	20	AAW25654	Carpinus betulus a	799	5	4.1	55	21	AAW53511	Human colon cancer
727	4.1	40	21	AAW09414	Hepatitis GB virus	800	5	4.1	55	21	AAW04659	Haem protein relat
728	4.1	40	22	AAW21694	Peptide #8128 enco	801	5	4.1	56	21	AAW70398	Protein encoded by
729	4.1	40	22	AAW38005	Peptide #12042 enc	802	5	4.1	56	22	AAW13990	Peptide #424 enco
730	4.1	41	20	AAW49769	Compact structure	803	5	4.1	56	22	AAW14420	Peptide #854 enco
731	4.1	41	20	AAW88087	Yeast 70 kD outer	804	5	4.1	56	22	AAW24354	Human EST encoded
732	4.1	41	21	AAW43830	Mitochondrial oute	805	5	4.1	56	22	AAW26396	Peptide #433 enco
733	4.1	41	21	AAW52276	M. pneumoniae ygd	806	5	4.1	56	22	AAW26833	Peptide #870 enco
734	4.1	41	22	AAW18903	Peptide #5337 enco	807	5	4.1	56	22	AAW01731	Peptide #413 enco
735	4.1	41	22	AAW31443	Peptide #5480 enco	808	5	4.1	56	22	AAW02147	Peptide #829 enco
736	4.1	41	22	AAW34283	Peptide #8320 enco	809	5	4.1	57	17	AAW88669	Human cytomegalovi
737	4.1	41	22	AAW45946	Transdominant effe	810	5	4.1	57	21	AAW94693	Human zslg93 epit
738	4.1	41	22	AAW35078	Yeast 70kD outer m	811	5	4.1	57	22	AAW15950	Peptide #2384 enco
739	4.1	42	21	AAW27049	zea mays protein f	812	5	4.1	57	22	AAW28453	Peptide #2490 enco
740	4.1	42	22	AAW76639	Human colon cancer	813	5	4.1	57	22	AAW37175	Peptide #11212 enc
741	4.1	43	20	AAW02746	Human secreted pro	814	5	4.1	57	22	AAW03688	Peptide #2370 enco

815	5	4.1	58	21	AAB40482	Human OREF ORF246	888	5	4.1	73	21	AAG00524	Human secreted pro
816	5	4.1	58	21	AAB43317	Human OREF ORF3081	889	5	4.1	73	22	AAM41980	Human polypeptide
817	5	4.1	58	21	AAG11425	Arabidopsis thalia	890	5	4.1	73	22	AAG74694	Human colon cancer
818	5	4.1	58	21	AAG50021	Arabidopsis thalia	891	5	4.1	74	20	AAV57463	Antimicrobial pept
819	5	4.1	58	22	AAM17066	Peptide #3500 enco	892	5	4.1	74	20	AAV57464	Antimicrobial pept
820	5	4.1	58	22	AAM17130	Peptide #3564 enco	893	5	4.1	74	20	AAV60440	Human normal bladd
821	5	4.1	58	22	AAM29560	Peptide #3597 enco	894	5	4.1	74	20	AAV11580	Human novel protei
822	5	4.1	58	22	AAM29623	Peptide #3660 enco	895	5	4.1	74	22	AAU14313	Human novel protei
823	5	4.1	58	22	AAM04768	Peptide #3450 enco	896	5	4.1	74	22	AAU14549	Amino acid sequenc
824	5	4.1	58	22	AAM04825	Peptide #3507 enco	897	5	4.1	75	18	AAW27980	Human secreted pro
825	5	4.1	58	22	AAG74158	Human colon cancer	898	5	4.1	75	20	AAV13046	IKK-alpha polypept
826	5	4.1	58	22	AAG74805	Human secreted pro	899	5	4.1	75	20	AAW96169	Human prostate can
827	5	4.1	59	20	AAV07888	Zeas may protein f	900	5	4.1	75	21	AAW56727	Human secreted pro
828	5	4.1	59	21	AAV25990	Peptide #9489 enco	901	5	4.1	75	21	AAW33729	Arabidopsis thalia
829	5	4.1	59	22	AAM35452	Human cytomagalovi	902	5	4.1	75	21	AAV22791	Zeas may protein f
830	5	4.1	59	22	AAB11464	CENP-B peptide. S	903	5	4.1	75	21	AAV27112	Arabidopsis thalia
831	5	4.1	60	14	AAV39273	Peptide #2019 enco	904	5	4.1	75	21	AAV45892	Peptide #2029 enco
832	5	4.1	60	22	AAM15585	Peptide #2114 enco	905	5	4.1	75	22	AAM15595	Peptide #2129 enco
833	5	4.1	60	22	AAM28077	Arabidopsis thalia	906	5	4.1	75	22	AAM03340	C glutamicum prote
834	5	4.1	60	22	AAM03329	Arabidopsis thalia	907	5	4.1	75	22	AAV90092	Human secreted pro
835	5	4.1	61	21	AAG48248	Arabidopsis thalia	908	5	4.1	76	21	AAV02755	Human zsig83 epit
836	5	4.1	61	21	AAG02241	Synechocystis tyro	909	5	4.1	76	20	AAV94694	A human alpha-heli
837	5	4.1	61	22	AAG76480	Chicken metallothi	910	5	4.1	76	21	AAV07613	Arabidopsis thalia
838	5	4.1	62	21	AAG03666	Human kidney relat	911	5	4.1	76	21	AAV07613	Arabidopsis thalia
839	5	4.1	62	21	AAG03666	Human secreted pro	912	5	4.1	76	21	AAV07613	Arabidopsis thalia
840	5	4.1	63	21	AAG20211	Arabidopsis thalia	913	5	4.1	76	21	AAV07613	Arabidopsis thalia
841	5	4.1	63	21	AAV77896	Arabidopsis thalia	914	5	4.1	76	21	AAV07613	Arabidopsis thalia
842	5	4.1	63	21	AAV57811	Synechocystis tyro	915	5	4.1	76	21	AAV07613	Arabidopsis thalia
843	5	4.1	63	22	AAM42583	Human kidney relat	916	5	4.1	76	22	AAV74264	Human secreted pro
844	5	4.1	63	22	AAV73406	Human gene 12-enco	917	5	4.1	76	22	AAV74264	Human colon cancer
845	5	4.1	64	14	AAV30639	Epitope of human C	918	5	4.1	77	18	AAW28041	Staphylococcus aur
846	5	4.1	64	19	AAV70476	Girdwood S.A.virus	919	5	4.1	77	20	AAV60199	Human endometrium
847	5	4.1	64	19	AAV70483	Sindbis virus E3 p	920	5	4.1	77	22	AAV74942	Human colon cancer
848	5	4.1	64	19	AAV70469	South African Arbo	921	5	4.1	78	20	AAV12633	Human PAP#4 prote
849	5	4.1	64	22	AAM20510	Peptide #6944 enco	922	5	4.1	78	20	AAV12633	Human 5' EST secre
850	5	4.1	64	22	AAM34524	Peptide #8561 enco	923	5	4.1	78	22	AAV75666	Human colon cancer
851	5	4.1	64	22	AAV35253	Peptide #9290 enco	924	5	4.1	79	20	AAV12993	Human secreted pro
852	5	4.1	65	21	AAV94689	Human zsig83 epit	925	5	4.1	79	21	AAV58924	Breast and ovarian
853	5	4.1	65	21	AAV26585	Arabidopsis thalia	926	5	4.1	79	21	AAV34138	Human secreted pro
854	5	4.1	65	21	AAG00533	Human secreted pro	927	5	4.1	79	21	AAV94690	Human zsig83 epit
855	5	4.1	65	22	AAM21559	Peptide #7993 enco	928	5	4.1	79	22	AAV25542	Human protein sequ
856	5	4.1	65	22	AAV37833	Peptide #11870 enco	929	5	4.1	79	22	AAV70689	Acanthamoeba caste
857	5	4.1	66	20	AAV12117	Human 5' EST secre	930	5	4.1	80	19	AAV38733	S. pneumoniae puri
858	5	4.1	66	21	AAV61695	Arabidopsis thalia	931	5	4.1	80	20	AAV60276	Human endometrium
859	5	4.1	66	21	AAV07619	Human secreted pro	932	5	4.1	80	21	AAV26771	Zeas may protein f
860	5	4.1	66	22	AAV34701	Peptide #8738 enco	933	5	4.1	81	20	AAV96168	IKK-alpha polypept
861	5	4.1	67	21	AAV03366	Human secreted pro	934	5	4.1	81	20	AAV88832	Polypeptide fragme
862	5	4.1	68	20	AAV60351	Human normal bladd	935	5	4.1	81	21	AAV32782	Eucalyptus grandis
863	5	4.1	68	21	AAV38479	Arabidopsis thalia	936	5	4.1	81	21	AAV07621	A human alpha-heli
864	5	4.1	68	22	AAV13610	Peptide #44 enco	937	5	4.1	81	21	AAV26584	Arabidopsis thalia
865	5	4.1	68	22	AAV26007	Peptide #44 enco	938	5	4.1	82	19	AAV74944	Human secreted pro
866	5	4.1	68	22	AAV01360	Peptide #42 enco	939	5	4.1	82	21	AAV37946	Chlamydia trachoma
867	5	4.1	68	22	AAV06379	Human foetal prote	940	5	4.1	82	21	AAV00770	Human secreted pro
868	5	4.1	68	22	AAV03059	Human gene 8 enco	941	5	4.1	82	21	AAV00772	Human secreted pro
869	5	4.1	68	22	AAV03090	Human gene 8 enco	942	5	4.1	82	21	AAV03269	Human secreted pro
870	5	4.1	69	19	AAV75015	Human secreted pro	943	5	4.1	82	22	AAV14726	Peptide #1160 enco
871	5	4.1	69	21	AAV27048	Zeas may protein f	944	5	4.1	82	22	AAV27149	Peptide #1186 enco
872	5	4.1	69	21	AAV01887	Human secreted pro	945	5	4.1	83	18	AAV20988	H. pylori cytoplas
873	5	4.1	70	18	AAV11327	S. pneumoniae prot	946	5	4.1	83	19	AAV74785	Human secreted pro
874	5	4.1	70	21	AAV53869	Human colon cancer	947	5	4.1	83	20	AAV12632	Human 5' EST secre
875	5	4.1	70	21	AAV57909	Arabidopsis thalia	948	5	4.1	83	21	AAV58037	DDC3 (dopa decarbo
876	5	4.1	70	22	AAU14295	Human novel protei	949	5	4.1	83	22	AAV92972	Human protein sequ
877	5	4.1	70	22	AAU14531	Human novel protei	950	5	4.1	83	22	AAV50241	Human breast cance
878	5	4.1	70	22	AAV67521	Human colon cancer	951	5	4.1	84	17	AAW01208	Serine protease pf
879	5	4.1	70	22	AAV77157	Human colon cancer	952	5	4.1	84	18	AAW00945	CMV500-4heptadREB
880	5	4.1	70	22	AAE01718	Human gene 9 enco	953	5	4.1	84	21	AAV16300	Eucalyptus grandis
881	5	4.1	71	21	AAV07611	A human alpha-heli	954	5	4.1	84	21	AAV58639	Arabidopsis thalia
882	5	4.1	72	19	AAV85793	S. pneumoniae deri	955	5	4.1	84	21	AAV57209	Arabidopsis thalia
883	5	4.1	72	21	AAV18896	Zeas may protein f	956	5	4.1	84	21	AAV02176	Human secreted pro
884	5	4.1	72	21	AAV25311	Zeas may protein f	957	5	4.1	84	21	AAV02380	Human secreted pro
885	5	4.1	72	21	AAV56876	Zeas may protein f	958	5	4.1	84	22	AAV76534	Human colon cancer
886	5	4.1	72	21	AAV76352	Fragment Of human	959	5	4.1	85	19	AAV59652	Flea serine protea
887	5	4.1	73	21	AAV40163	Human secreted pro	960	5	4.1	85	20	AAV59643	Amino acid sequenc

DE Human secreted protein encoded by gene 17 clone HPMBQ91.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX WO9840483-A2.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04858.

XX 19-DEC-1997; 97US-0068368.

XX 14-MAR-1997; 97US-0040710.

XX 30-MAY-1997; 97US-0048100.

XX 30-MAY-1997; 97US-0048189.

XX 30-MAY-1997; 97US-0048357.

XX 30-MAY-1997; 97US-0050934.

XX 06-JUN-1997; 97US-0048970.

XX 05-SEP-1997; 97US-0057765.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;

XX Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;

XX Wei YF, Young PE, Zeng Z;

XX WPI: 1998-520811/44.

XX N-PSDB; AAV34302.

XX Isolated human poly(nucleotide(s)) encoding secretory peptide(s) -

XX used to develop products for the diagnosis and treatment of e.g.

XX inflammation, cancers, CNS disorders or immune system disorders

XX Claim 1; Page 162-163; 20lpp; English.

XX This sequence represents a secreted human protein encoded by the gene

XX clone detailed in the descriptor line. The gene can be used to generate

XX fusion proteins by linking to the gene to a human immunoglobulin Fc

XX portion (e.g. AAV34277) for increasing the stability of the fused

XX protein as compared to the human protein only.

XX The invention relates to 28 novel genes and their fragments (nucleic

XX acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)

XX which are useful for preventing, treating or ameliorating medical

XX conditions e.g. by protein or gene therapy. Also, pathological

XX conditions can be diagnosed by determining the amount of the new

XX polypeptides in a sample or by determining the presence of mutations in

XX the new polynucleotides. Specific uses are described for each of the 28

XX polynucleotides, based on which tissues they are most highly expressed in

XX (see AAV34286 for described uses).

XX Sequence 121 AA;

XX SQ

RESULT 3

AAW97213

ID AAW97213 standard; Protein; 121 AA.

XX AAW97213;

XX 07-MAY-1999 (first entry)

XX A human zneurokl polypeptide.

XX Human; zneurokl; neurokinin B; prohormone convertase; cell growth;

XX modulation; inflammation; noinception; emesis; contraction;

XX hormone secretion; DNA synthesis; inositol phosphate turnover;

XX arachidonate release; phospholipase-C activation; gastric emptying;

XX human neutrophil activation; ADCC capability;

XX superoxide anion production; gene therapy.

XX Homo sapiens.

XX WO9855612-A1.

XX 10-DEC-1998.

XX 28-MAY-1998; 98WO-US10842.

XX 02-JUN-1997; 97US-0048290.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO;

XX WPI: 1999-070268/06.

XX N-PSDB; AAX15447.

XX New isolated neurokinin polypeptides, zneurokl - used to develop

XX products for modulating e.g. inflammation, noinception, emesis,

XX muscle contraction, hormone secretion, DNA synthesis or cell growth

XX Claim 3; Page 76-77; 100pp; English.

XX The present sequence represents a human zneurokl polypeptide. The

XX polypeptide releases a neurokinin B polypeptide in the presence

XX of a prohormone convertase capable of cleaving dibasic amino

XX acids. The zneurokl polypeptides can be used for modulating inflammation,

XX noinception or emesis. The polypeptides, fragments, fusion proteins,

XX agonists, antagonists or antibodies may also modulate contraction,

XX hormone secretion, DNA synthesis or cell growth, inositol phosphate

XX turnover, arachidonate release, phospholipase-C activation, gastric

XX emptying, human neutrophil activation or ADCC capability, or superoxide

XX anion production. The polynucleotides can also be used for gene therapy.

XX The products can also be used for detection, diagnosis and screening

XX assays.

XX Sequence 121 AA;

XX SQ

Query Match 54.5%; Score 66; DB 20; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.1e-57;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLFTAILAFSLAQSGFVCKEPEEVVPGGSKRDPDLYQLLQRLFKSHSSLEGL 60

|||||

Db 1 mrmlftailafslaqsgfvcckepcvpggskrdpdyqlqlrfkshsslegl 60

QY 61 LKALSQ 66

|||||

Db 61 lkalsq 66

RESULT 4

AAW74413

Query Match 54.5%; Score 66; DB 19; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.1e-57;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLFTAILAFSLAQSGFVCKEPEEVVPGGSKRDPDLYQLLQRLFKSHSSLEGL 60

|||||

Db 1 mrmlftailafslaqsgfvcckepcvpggskrdpdyqlqlrfkshsslegl 60

QY 61 LKALSQ 66

|||||

Db 61 lkalsq 66

Db 61 lkalsq 66

RESULT 6
AAW96144
ID AAW96144 standard; Protein; 122 AA.
XX AC AAW96144;
XX DT 27-APR-1999 (first entry)
XX DE Human preprotachykinin B.
XX KW Preprotachykinin B; PPT-B; neoplastic disorder;
KW neurological disorder; Alzheimer's disease; amnesia;
KW cerebral neoplasms; dementia; depression; Down's syndrome;
KW Huntington's disease; multiple sclerosis; Parkinson's disease;
KW paranoid psychoses; schizophrenia; Tourette's disorder; angina;
KW anaphylactic shock; asthma; cardiovascular shock;
KW myocardial infarction; migraine.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 104
FT /label= Leu, Ser or Trp
XX PN WO9857986-A2.
XX PD 23-DEC-1998.
XX XX 19-JUN-1998; 98WO-US12855.
XX XX 19-JUN-1997; 97US-0879995.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Hillman JJ, Kaser MR, Lal P;
XX WPI: 1999-080948/07.
XX N-PSDB; AAX08906.
XX PT New human preprotachykinin B - useful for treating neurological
XX disorders and cancer
XX PS Claim 1; Page 48-49; 57pp; English.
XX CC Human preprotachykinin B (PPT-B) can be used to treat a
CC neurological disorder. Antagonists of PPT-B can also be used in
CC the treatment of neoplastic disorders. Particular neurological,
CC disorders include akathisia, Alzheimer's disease, amnesia,
CC amyotrophic lateral sclerosis, bipolar disorder, cataplexy,
CC cerebral neoplasms, dementia, depression, Down's syndrome, tardive
CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,
CC neurofibromatosis, Parkinson's disease, paranoid psychoses,
CC schizophrenia, and Tourette's disorder. PPT-B or its agonist can
CC also be used to treat angina, anaphylactic shock, arrhythmias,
CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,
CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.
XX SQ Sequence 122 AA;

Query Match 54.5%; Score 66; DB 20; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLFTAILAFSLAQSGAVCKPEQEVPGGRSKRDPDLYQLLQRLFKSHSLGL 60
|||||
Db 1 mrimlftailafslaqsgavckpeevpggrskrdpdyqlrlfkshsslegl 60
|||||

QY 61 LKALSQ 66
|||||

Db 61 lkalsq 66

RESULT 7
AAB33445
ID AAB33445 standard; Protein; 135 AA.
XX AC AAB33445;
XX DT 29-JAN-2001 (first entry)
XX DE Human PRO1155 protein UNQ585 SEQ ID NO:157.
XX KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antianastemic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX OS Homo sapiens.
XX XX WO200053758-A2.
XX PD 14-SEP-2000.
XX XX 02-MAR-2000; 2000WO-US05841.
XX PF 08-MAR-1999; 99WO-US05028.
XX PR 10-MAR-1999; 99US-0123618.
XX PR 12-MAR-1999; 99US-0123957.
XX PR 23-MAR-1999; 99US-0125775.
XX PR 12-APR-1999; 99US-0128849.
XX PR 20-APR-1999; 99WO-US08615.
XX PR 28-APR-1999; 99US-0131445.
XX PR 04-MAY-1999; 99US-0132371.
XX PR 14-MAY-1999; 99US-0134287.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 08-SEP-1999; 99WO-US20594.
XX PR 13-SEP-1999; 99WO-US20944.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 15-SEP-1999; 99WO-US21547.
XX PR 05-OCT-1999; 99WO-US23089.
XX PR 29-OCT-1999; 99US-0162506.
XX PR 29-OCT-1999; 99WO-US28214.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 30-NOV-1999; 99WO-US28409.
XX PR 01-DEC-1999; 99WO-US28301.
XX PR 01-DEC-1999; 99WO-US28634.
XX PR 02-DEC-1999; 99WO-US28551.
XX PR 02-DEC-1999; 99WO-US28564.
XX PR 16-DEC-1999; 99WO-US28565.
XX PR 20-DEC-1999; 99WO-US30095.
XX PR 20-DEC-1999; 99WO-US30999.
XX PR 30-DEC-1999; 99WO-US31274.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 06-JAN-2000; 2000WO-US00277.
XX PR 11-FEB-2000; 2000WO-US03376.
XX PR 18-FEB-2000; 2000WO-US03565.
XX PR 18-FEB-2000; 2000WO-US04341.


```
PR 25-JUN-1998; 98US-00906595.
PR 25-JUN-1998; 98US-00906596.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091344.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-010634.
PR 12-JAN-1999; 99US-0115565.
PR XX
PA (GETH ) GENENTECH INC.
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI; 2000-072883/06.
DR N-PSDB; AAZ65085.
DR
```

Membrane-bound proteins and related nucleotide sequences -
claim 12; Fig 254; 822pp; English.
The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

XX Sequence 135 AA;
SQ

Query Match 54.5%; Score 66; DB 21; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.2e-57;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTALAFSLAQSGAVCKEPQEEVVPVGGSRKDPDLYQLLORLFKSHSLEGL 60
|||||
Db 1 mrimllftalafslaqsgavckepqeevvpvggrskrdpdyqlqlrkfshssleagl 60
|||||

QY 61 LKALSQ 66
|||||
Db 61 lkalsq 66

RESULT 9
AAB65262
ID AAB65262 standard; Protein; 135 AA.
XX
AC AAB65262;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1155 (UNQ585) protein sequence SEQ ID NO:359.
KW Human; secreted and transmembrane protein; PRO: cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR

PD 20-JAN-1999.
XX
PF 26-JUN-1998; 98EP-0305066.
XX
XX 14-JUL-1997; 97EP-0305215.
XX
PA (HUMA-) HUMAN GENOME SCI.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Duckworth DM, Hastings GA, Ruben SM;
PI
XX WPI; 1999-083570/08.
XX
XX New human neurokinin B precursor (HPMBQ91) polypeptides and
PT polynucleotide - useful as diagnostic reagents and for prevention
PT and treatment of neuronal, metabolic, inflammatory and
PT gastrointestinal disorders, and cancers
XX
XX Claim 14; Page 15; 18pp; English.
XX
CC This sequence is the human neurokinin B precursor HPMBQ91 of the
CC invention. HPMBQ91 polypeptides and polynucleotides are useful for
CC diagnosing susceptibility to diseases associated with HPMBQ91 protein
CC imbalance by determining HPMBQ91 polypeptide expression levels. HPMBQ91
CC polypeptides can be used to screen for agonists and antagonists by
CC measuring the binding to HPMBQ91, and observing the stimulation or
CC inhibition of HPMBQ91 function. These can be used in treatment to
CC activate or inhibit HPMBQ91 activity to treat conditions associated with
CC a lack of HPMBQ91 protein. Gene therapy may also be used to affect
CC endogenous HPMBQ91 polypeptide expression. HPMBQ91 antibodies are useful
CC for inducing an immune response to immunise and prevent disease, and for
CC isolating HPMBQ91 clones or purifying the polypeptides by affinity
CC chromatography. HPMBQ91 polypeptides can be administered directly or as a
CC vaccine to inoculate against disease. Diseases diagnosed, prevented or
CC treated include: neuronal disorders; CNS related disorders;
CC gastrointestinal and cardiovascular disorders; metabolic disorders
CC including diabetes and obesity; smooth muscle disorders; inflammatory
CC disorders; and cancers including adenomas, leiomyomas, liposarcomas,
CC melanomas, pulmonary chondroid hamartomas, lung, prostate and breast
CC cancer. The HPMBQ91 polypeptide is also useful for mapping the gene to a
CC chromosome, allowing gene inheritance to be studied through linkage
CC analysis, and tissue localisation studies, for determining HPMBQ91
CC expression patterns.
XX
SQ Sequence 39 AA;
Query Match 22.3%; Score 27; DB 20; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e-19; Mismatches 0; Gaps 0;
Matches 27; Conservative 0; Indels 0; Indels 0; Gaps 0;
QY 40 DPDLYQLLRLFRKSHSLEGLLKALSQ 66
DB 1 dpdlyqlrlfrkshsleglkalsq 27
RESULT 12
AAW75249
ID AAW75249 standard; Protein; 36 AA.
XX
AC AAW75249;
XX
XX 29-JAN-1999 (first entry)
XX
XX Fragment of human secreted protein encoded by gene 17.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX Homo sapiens.
XX
XX WO9840483-A2.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-US04858.
XX
XX 19-DEC-1997; 97US-0068368.
PR 14-MAR-1997; 97US-0040710.
PR 14-MAR-1997; 97US-0040762.
PR 30-MAY-1997; 97US-0048100.
PR 30-MAY-1997; 97US-0048189.
PR 30-MAY-1997; 97US-0048357.
PR 30-MAY-1997; 97US-0050934.
PR 06-JUN-1997; 97US-0048970.
PR 05-SEP-1997; 97US-0057765.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
PI Wei YF, Young PE, Zeng Z;
XX
XX WPI; 1998-520811/44.
DR N-PSDB; AAV34302.
XX
XX Isolated human polynucleotide(s) encoding secretory peptide(s) -
PT used to develop products for the diagnosis and treatment of e.g.
PT inflammation, cancers, CNS disorders or immune system disorders
XX
XX Disclosure; Page 19; 201pp; English.
XX
XX This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule designated Gene 17 (AAV34302). The gene
CC can be used to generate fusion proteins by linking to the gene to a
CC human immunoglobulin Fc portion (e.g. AAV34277) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 28 novel genes and their fragments (nucleic
CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 28
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34286 for described uses).
XX
SQ Sequence 36 AA;
Query Match 19.0%; Score 23; DB 19; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 0; Indels 0; Gaps 0;
QY 90 MGKRSVQPSDPTDNOENVPISFG 112
DB 14 mgkrsvqpsdptdncvnpisfg 36
RESULT 13
AAW75250
ID AAW75250 standard; Protein; 15 AA.
XX
AC AAW75250;
XX
XX 29-JAN-1999 (first entry)
XX
XX Fragment of human secreted protein encoded by gene 17.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; fetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

W09840483-A2.

17-SEP-1998.

12-MAR-1998; 98WO-US04858.

19-DEC-1997; 97US-0068368.

14-MAR-1997; 97US-0040710.

30-MAY-1997; 97US-0040762.

30-MAY-1997; 97US-0048100.

30-MAY-1997; 97US-0048189.

30-MAY-1997; 97US-0048357.

06-JUN-1997; 97US-0050934.

05-SEP-1997; 97US-0048970.

05-SEP-1997; 97US-0057765.

(HUMA-) HUMAN GENOME SCI INC.

Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;

Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;

Wei YF, Young PE, Zeng Z;

WPI; 1998-520811/44.

N-PSDB; AAV34302.

Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders

Disclosure: Page 19; 20lpp; English.

This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule designated Gene 17 (AAV34302). The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 28 novel genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 28 polynucleotides, based on which tissues they are most highly expressed in (see AAV34286 for described uses).

Sequence 15 AA;

Query Match 8.3%; Score 10; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.0053;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVFG 88

|||||

Db 1 krdmhdfvfg 10

RESULT 14

AAW97214

ID AAW97214 standard; Protein; 92 AA.

XX

AC AAW97214;

XX

DT

XX

DE

XX

KW

KW

KW

KW

KW

KW

KW

KW

OS

OS

XX

PN

XX

PD

XX

XX

PF

XX

XX

PR

XX

XX

PA

XX

XX

PI

XX

XX

DR

DR

DR

XX

PT

XX

PT

XX

PS

XX

CC

CC

07-MAY-1999 (first entry)

A murine homologue of human zneurok1 polypeptide.

Human; zneurok1; neurokinin B; prohormone convertase; cell growth; modulation; inflammation; noinception; emesis; contraction; hormone secretion; DNA synthesis; inositol phosphate turnover; arachidonate release; phospholipase-C activation; gastric emptying; human neutrophil activation; ADCC capability; superoxide anion production; gene therapy.

Mus sp.

W09855612-A1.

10-DEC-1998.

28-MAY-1998; 98WO-US10842.

02-JUN-1997; 97US-0048290.

(ZYMO) ZYMOGENETICS INC.

Sheppard PO;

WPI; 1999-070268/06.

N-PSDB; AAX15448.

New isolated neurokinin polypeptides, zneurok1 - used to develop products for modulating e.g. inflammation, noinception, emesis, muscle contraction, hormone secretion, DNA synthesis or cell growth

Example 1; Page 87; 100pp; English.

The present sequence represents a murine homologue of human zneurok1. The zneurok1 polypeptide releases a neurokinin B polypeptide in the presence of a prohormone convertase capable of cleaving dibasic amino acids. The zneurok1 polypeptides can be used for modulating inflammation, noinception or emesis. The polypeptides, fragments, fusion proteins, agonists, antagonists or antibodies may also modulate contraction, hormone secretion, DNA synthesis or cell growth, inositol phosphate turnover, arachidonate release, phospholipase-C activation, gastric emptying, human neutrophil activation or ADCC capability, or superoxide anion production. The polynucleotides can also be used for gene therapy. The products can also be used for detection, diagnosis and screening assays.

Sequence 92 AA;

Query Match 8.3%; Score 10; DB 20; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVFG 88

|||||

Db 80 krdmhdfvfg 89

RESULT 15

AAW96146

ID AAW96146 standard; Protein; 116 AA.

XX

AC AAW96146;

XX

DT 27-APR-1999 (first entry)

XX

DE

XX

XX

Rat preprotachykinin B.

Preprotachykinin B; PPT-B; neoplastic disorder;

neurological disorder; Alzheimer's disease; amnesia;

cerebral neoplasms; dementia; depression; Down's syndrome;

KW Huntington's disease; multiple sclerosis; Parkinson's disease;
 KW paranoic psychoses; schizophrenia; Tourette's disorder; angina;
 KW anaphylactic shock; asthma; cardiovascular shock;
 XX myocardial infarction; migraine.

OS - Rattus rattus.

XX WO9857986-A2.

XX PD 23-DEC-1998.

XX PF 19-JUN-1998; 98WO-US12855.

XX PR 19-JUN-1997; 97US-0879995.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Hillman JJ, Kaser MR, Lal P;

XX WPI; 1999-080948/07.

XX New human preprotachykinin B - useful for treating neurological
 PT disorders and cancer

XX Disclosure; Figure 2; 57pp; English.

XX Human preprotachykinin B (AAW96144) (PPT-B) can be used to treat a
 CC neurological disorder. Antagonists of PPT-B can also be used in
 CC the treatment of neoplastic disorders. Particular neurological,
 CC disorders include akathisia, Alzheimer's disease, amnesia,
 CC amyotrophic lateral sclerosis, bipolar disorder, catatonia,
 CC cerebral neoplasms, dementia, depression, Down's syndrome, tardive
 CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,
 CC neurofibromatosis, Parkinson's disease, paranoic psychoses,
 CC schizophrenia, and Tourette's disorder. PPT-B or its agonist can
 CC also be used to treat angina, anaphylactic shock, arrhythmias,
 CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,
 CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.

XX Sequence 116 AA;

Query Match 8.3%; Score 10; DB 20; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVVG 88
 Db 80 krdmhdffvg 89

Search completed: May 3, 2002, 12:28:31
 Job time: 223 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:26:43 ; Search time 12.76 Seconds
(without alignments)
213.393 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRMLLFTALFSLAQSG.....DVNOENVPSGILKYPPRAE 121

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES											
Result No.	Score	Query Match	Length	DB ID	Description						
1	66	54.5	122	2	US-08-879-995A-1	Sequence 1, Appli					
2	66	54.5	122	3	US-09-215-096-1	Sequence 1, Appli					
3	10	8.3	116	2	US-08-879-995A-4	Sequence 4, Appli					
4	10	8.3	116	3	US-09-215-096-4	Sequence 4, Appli					
5	10	8.3	126	2	US-08-879-995A-3	Sequence 3, Appli					
6	10	8.3	126	3	US-09-215-096-3	Sequence 3, Appli					
7	8	6.6	10	1	US-07-899-205-3	Sequence 3, Appli					
8	8	6.6	10	1	US-08-184-935-10	Sequence 10, Appli					
9	8	6.6	10	1	US-08-269-288-4	Sequence 4, Appli					
10	8	6.6	10	1	US-08-338-484-3	Sequence 3, Appli					
11	8	6.6	10	1	US-08-175-432-3	Sequence 3, Appli					
12	8	6.6	10	1	US-08-462-413-4	Sequence 4, Appli					
13	8	6.6	10	1	US-08-391-910-4	Sequence 4, Appli					
14	8	6.6	10	1	US-08-418-994-4	Sequence 4, Appli					
15	8	6.6	10	1	US-08-391-814-4	Sequence 4, Appli					
16	8	6.6	10	1	US-08-167-870-3	Sequence 3, Appli					
17	8	6.6	10	1	US-08-462-415-4	Sequence 4, Appli					
18	8	6.6	10	1	US-08-463-874-4	Sequence 4, Appli					
19	8	6.6	10	1	US-08-318-391-4	Sequence 4, Appli					
20	8	6.6	10	2	US-08-496-118-3	Sequence 3, Appli					
21	8	6.6	10	2	US-07-737-371E-74	Sequence 74, Appli					
22	8	6.6	10	4	US-08-257-966-4	Sequence 4, Appli					
23	7	5.8	590	1	US-08-221-817-14	Sequence 14, Appli					
24	7	5.8	590	1	US-08-454-439-14	Sequence 14, Appli					
25	7	5.8	590	4	US-08-464-954A-5	Sequence 5, Appli					
26	7	5.8	590	5	PCT-US94-10487-14	Sequence 14, Appli					
27	6	5.0	10	2	US-07-737-371E-43	Sequence 43, Appli					

28	6	5.0	10	2	US-07-737-371E-44	Sequence 44, Appli
29	6	5.0	26	4	US-08-789-333F-18	Sequence 18, Appli
30	6	5.0	26	4	US-09-169-015-28	Sequence 28, Appli
31	6	5.0	26	4	US-09-133-944-18	Sequence 18, Appli
32	6	5.0	48	4	US-08-836-075A-22	Sequence 22, Appli
33	6	5.0	67	2	US-08-637-759B-164	Sequence 164, App
34	6	5.0	67	2	US-08-871-355A-164	Sequence 164, App
35	6	5.0	113	2	US-08-710-330A-2	Sequence 2, Appli
36	6	5.0	139	1	US-08-680-726A-66	Sequence 66, Appli
37	6	5.0	139	4	US-09-092-409-66	Sequence 66, Appli
38	6	5.0	152	3	US-08-992-176-10	Sequence 10, Appli
39	6	5.0	153	3	US-08-992-176-7	Sequence 7, Appli
40	6	5.0	157	4	US-09-267-177-19	Sequence 19, Appli
41	6	5.0	177	2	US-08-867-030B-16	Sequence 16, Appli
42	6	5.0	177	5	PCT-US95-06119-16	Sequence 16, Appli
43	6	5.0	193	1	US-08-248-466B-14	Sequence 14, Appli
44	6	5.0	204	1	US-08-185-432-8	Sequence 8, Appli
45	6	5.0	209	2	US-08-870-518-10	Sequence 10, Appli
46	6	5.0	210	2	US-08-781-560-4	Sequence 4, Appli
47	6	5.0	210	2	US-08-933-750C-6	Sequence 6, Appli
48	6	5.0	210	3	US-08-792-014-4	Sequence 4, Appli
49	6	5.0	210	4	US-09-234-613-6	Sequence 6, Appli
50	6	5.0	210	4	US-09-443-948-4	Sequence 4, Appli
51	6	5.0	212	1	US-08-158-353-4	Sequence 4, Appli
52	6	5.0	212	2	US-08-753-159A-4	Sequence 4, Appli
53	6	5.0	212	3	US-09-133-735-4	Sequence 4, Appli
54	6	5.0	212	4	US-09-196-293-11	Sequence 11, Appli
55	6	5.0	212	4	US-08-209-603E-11	Sequence 11, Appli
56	6	5.0	212	4	US-08-235-836C-34	Sequence 34, Appli
57	6	5.0	265	2	US-08-898-779-2	Sequence 2, Appli
58	6	5.0	265	2	US-08-898-779-4	Sequence 2, Appli
59	6	5.0	265	4	US-09-224-502-2	Sequence 2, Appli
60	6	5.0	265	4	US-09-224-502-4	Sequence 4, Appli
61	6	5.0	276	2	US-08-846-782-7	Sequence 7, Appli
62	6	5.0	276	2	US-08-846-782-77	Sequence 77, Appli
63	6	5.0	287	4	US-09-105-697-7	Sequence 7, Appli
64	6	5.0	287	4	US-09-105-697-8	Sequence 8, Appli
65	6	5.0	288	4	US-09-105-697-3	Sequence 3, Appli
66	6	5.0	289	4	US-09-105-697-2	Sequence 2, Appli
67	6	5.0	297	3	US-09-173-581-1	Sequence 1, Appli
68	6	5.0	297	4	US-09-420-915-1	Sequence 1, Appli
69	6	5.0	303	1	US-08-185-432-5	Sequence 5, Appli
70	6	5.0	310	2	US-08-484-956-88	Sequence 88, Appli
71	6	5.0	310	2	US-08-757-653-88	Sequence 88, Appli
72	6	5.0	315	2	US-08-484-956-91	Sequence 91, Appli
73	6	5.0	315	2	US-08-757-653-91	Sequence 91, Appli
74	6	5.0	320	2	US-08-757-653-163	Sequence 163, App
75	6	5.0	320	2	US-08-823-516-61	Sequence 61, Appli
76	6	5.0	320	3	US-08-759-038-102	Sequence 102, App
77	6	5.0	320	3	US-08-758-314-102	Sequence 102, App
78	6	5.0	322	2	US-08-484-956-89	Sequence 89, Appli
79	6	5.0	322	2	US-08-757-653-89	Sequence 89, Appli
80	6	5.0	335	1	US-08-289-699A-4	Sequence 4, Appli
81	6	5.0	335	2	US-08-878-283-4	Sequence 4, Appli
82	6	5.0	348	4	US-09-113-536-2	Sequence 2, Appli
83	6	5.0	348	5	PCT-US95-05785-2	Sequence 2, Appli
84	6	5.0	359	1	US-08-148-209A-4	Sequence 4, Appli
85	6	5.0	366	2	US-08-846-762-78	Sequence 78, Appli
86	6	5.0	381	2	US-08-867-057-1	Sequence 1, Appli
87	6	5.0	381	2	US-09-128-369-1	Sequence 1, Appli
88	6	5.0	390	3	US-08-961-564A-2	Sequence 2, Appli
89	6	5.0	439	4	US-08-952-457-2	Sequence 2, Appli
90	6	5.0	439	4	US-08-952-457-3	Sequence 3, Appli
91	6	5.0	441	4	US-09-625-188-4	Sequence 4, Appli
92	6	5.0	454	2	US-03-159-385-1	Sequence 1, Appli
93	6	5.0	454	4	US-09-186-277-1	Sequence 1, Appli
94	6	5.0	455	4	US-09-362-473-6	Sequence 6, Appli
95	6	5.0	459	2	US-08-870-518-1	Sequence 1, Appli
96	6	5.0	459	2	US-08-870-518-2	Sequence 2, Appli
97	6	5.0	483	3	US-08-889-841B-31	Sequence 31, Appli
98	6	5.0	486	4	US-08-906-743-4	Sequence 4, Appli
99	6	5.0	487	3	US-08-889-841B-33	Sequence 33, Appli
100	6	5.0	516	2	US-08-676-166A-2	Sequence 2, Appli

101	6	5.0	528	2	US-08-484-956-90	Sequence 90, Appl	174	6	5.0	833	2	US-08-757-653-190	Sequence 190, Appl
102	6	5.0	528	2	US-08-757-653-90	Sequence 90, Appl	175	6	5.0	833	2	US-08-599-491-8	Sequence 8, Appl1
103	6	5.0	548	2	US-08-484-956-86	Sequence 86, Appl	176	6	5.0	833	2	US-08-756-386-8	Sequence 8, Appl1
104	6	5.0	548	2	US-08-757-653-86	Sequence 86, Appl	177	6	5.0	833	2	US-08-823-516-8	Sequence 8, Appl1
105	6	5.0	556	4	US-08-687-590-24	Sequence 24, Appl	178	6	5.0	833	2	US-08-823-516-66	Sequence 66, Appl
106	6	5.0	563	4	US-08-906-743-2	Sequence 2, Appl1	179	6	5.0	833	2	US-08-823-516-69	Sequence 69, Appl
107	6	5.0	576	1	US-08-221-817-13	Sequence 13, Appl	180	6	5.0	833	2	US-08-823-516-71	Sequence 71, Appl
108	6	5.0	576	1	US-08-221-817-22	Sequence 22, Appl	181	6	5.0	833	3	US-08-682-853A-8	Sequence 8, Appl1
109	6	5.0	576	1	US-08-454-439-13	Sequence 13, Appl	182	6	5.0	833	3	US-08-759-038-8	Sequence 8, Appl1
110	6	5.0	576	1	US-08-454-439-22	Sequence 22, Appl	183	6	5.0	833	3	US-08-759-038-107	Sequence 107, App
111	6	5.0	576	1	US-08-464-954A-6	Sequence 6, Appl1	184	6	5.0	833	3	US-08-759-038-130	Sequence 130, App
112	6	5.0	576	5	PCR-US94-10487-13	Sequence 13, Appl	185	6	5.0	833	3	US-08-759-038-132	Sequence 132, App
113	6	5.0	576	5	PCR-US94-10487-22	Sequence 22, Appl	186	6	5.0	833	3	US-08-758-314-8	Sequence 8, Appl1
114	6	5.0	584	1	US-08-426-819A-36	Sequence 36, Appl	187	6	5.0	833	3	US-08-758-314-107	Sequence 107, App
115	6	5.0	622	1	US-08-426-819A-35	Sequence 35, Appl	188	6	5.0	833	3	US-08-758-314-130	Sequence 130, App
116	6	5.0	628	3	US-08-776-271-2	Sequence 2, Appl1	189	6	5.0	833	3	US-08-758-314-132	Sequence 132, App
117	6	5.0	628	4	US-09-213-035-2	Sequence 2, Appl1	190	6	5.0	948	1	US-08-698-551-14	Sequence 14, Appl
118	6	5.0	632	1	US-08-221-817-11	Sequence 11, Appl	191	6	5.0	948	2	US-08-602-228-14	Sequence 14, Appl
119	6	5.0	632	1	US-08-454-439-11	Sequence 11, Appl	192	6	5.0	948	2	US-08-533-901B-14	Sequence 14, Appl
120	6	5.0	632	5	PCR-US94-10487-11	Sequence 11, Appl	193	6	5.0	948	2	US-08-839-032A-14	Sequence 14, Appl
121	6	5.0	695	2	US-08-484-956-87	Sequence 87, Appl	194	6	5.0	948	2	US-08-839-031A-14	Sequence 14, Appl
122	6	5.0	695	2	US-08-757-653-87	Sequence 87, Appl	195	6	5.0	948	5	PCR-US95-12724-14	Sequence 14, Appl
123	6	5.0	737	1	US-08-185-432-2	Sequence 2, Appl1	196	6	5.0	1275	3	US-09-120-513-2	Sequence 2, Appl1
124	6	5.0	737	1	US-08-185-432-4	Sequence 4, Appl1	197	6	5.0	1275	4	US-09-450-103-2	Sequence 2, Appl1
125	6	5.0	810	4	US-09-587-856-2	Sequence 2, Appl1	198	6	5.0	7257	3	US-09-335-409-5	Sequence 5, Appl1
126	6	5.0	830	1	US-07-977-434-6	Sequence 6, Appl1	199	5	4.1	5	1	US-08-127-904-1	Sequence 1, Appl1
127	6	5.0	830	1	US-08-458-819-6	Sequence 6, Appl1	200	5	4.1	5	5	PCR-US94-10475-1	Sequence 1, Appl1
128	6	5.0	830	5	PCR-US91-07035-6	Sequence 6, Appl1	201	5	4.1	8	1	US-07-876-280-11	Sequence 11, Appl
129	6	5.0	831	1	US-08-073-384C-5	Sequence 5, Appl1	202	5	4.1	8	1	US-07-968-781A-61	Sequence 61, Appl
130	6	5.0	831	1	US-08-254-359A-5	Sequence 5, Appl1	203	5	4.1	8	1	US-08-158-232-14	Sequence 14, Appl
131	6	5.0	831	1	US-08-483-043-5	Sequence 5, Appl1	204	5	4.1	8	1	US-08-304-626-14	Sequence 14, Appl
132	6	5.0	831	1	US-08-481-238-5	Sequence 5, Appl1	205	5	4.1	8	1	US-08-316-301A-15	Sequence 15, Appl
133	6	5.0	831	2	US-08-471-066B-5	Sequence 5, Appl1	206	5	4.1	8	3	US-08-611-928-14	Sequence 14, Appl
134	6	5.0	831	2	US-08-484-956-5	Sequence 5, Appl1	207	5	4.1	8	4	US-09-076-137-15	Sequence 15, Appl
135	6	5.0	831	2	US-08-757-653-5	Sequence 5, Appl1	208	5	4.1	8	4	US-09-139-802-104	Sequence 104, App
136	6	5.0	831	2	US-08-599-491-5	Sequence 5, Appl1	209	5	4.1	8	5	PCR-US92-03624-15	Sequence 15, Appl
137	6	5.0	831	2	US-08-756-386-5	Sequence 5, Appl1	210	5	4.1	8	2	US-08-599-602-38	Sequence 38, Appl
138	6	5.0	831	2	US-08-823-516-5	Sequence 5, Appl1	211	5	4.1	9	3	US-09-197-816-38	Sequence 38, Appl
139	6	5.0	831	3	US-08-682-853A-5	Sequence 5, Appl1	212	5	4.1	11	4	US-09-196-293-7	Sequence 7, Appl1
140	6	5.0	831	3	US-08-759-038-5	Sequence 5, Appl1	213	5	4.1	11	4	US-08-209-603E-7	Sequence 7, Appl1
141	6	5.0	831	3	US-08-758-314-5	Sequence 5, Appl1	214	5	4.1	11	6	5194592-77	Patent No. 5194592
142	6	5.0	832	1	US-07-977-434-2	Sequence 2, Appl1	215	5	4.1	14	1	US-08-232-453A-40	Sequence 40, Appl
143	6	5.0	832	1	US-08-156-020-2	Sequence 2, Appl1	216	5	4.1	14	1	US-08-232-453A-46	Sequence 46, Appl
144	6	5.0	832	1	US-08-156-020-4	Sequence 4, Appl1	217	5	4.1	14	1	US-08-232-453A-46	Sequence 46, Appl
145	6	5.0	832	1	US-08-156-020-6	Sequence 6, Appl1	218	5	4.1	14	1	US-07-977-696C-39	Sequence 39, Appl
146	6	5.0	832	1	US-08-156-020-8	Sequence 8, Appl1	219	5	4.1	14	1	US-08-129-930B-39	Sequence 39, Appl
147	6	5.0	832	1	US-08-156-020-10	Sequence 10, Appl	220	5	4.1	14	2	US-08-529-190B-76	Sequence 76, Appl
148	6	5.0	832	1	US-08-073-384C-4	Sequence 4, Appl1	221	5	4.1	14	4	US-08-134-346A-26	Sequence 26, Appl
149	6	5.0	832	1	US-08-254-359A-4	Sequence 4, Appl1	222	5	4.1	15	2	US-08-726-306A-55	Sequence 55, Appl
150	6	5.0	832	1	US-08-483-043-4	Sequence 4, Appl1	223	5	4.1	16	2	US-08-434-834-7	Sequence 7, Appl1
151	6	5.0	832	1	US-08-458-819-2	Sequence 2, Appl1	224	5	4.1	17	2	US-08-434-834-6	Sequence 6, Appl1
152	6	5.0	832	1	US-08-481-238-4	Sequence 4, Appl1	225	5	4.1	17	4	US-08-905-223-18	Sequence 18, Appl
153	6	5.0	832	2	US-08-471-066B-4	Sequence 4, Appl1	226	5	4.1	18	1	US-07-855-412B-3	Sequence 3, Appl1
154	6	5.0	832	2	US-08-484-956-4	Sequence 4, Appl1	227	5	4.1	18	2	US-08-308-887A-3	Sequence 3, Appl1
155	6	5.0	832	2	US-08-757-653-4	Sequence 4, Appl1	228	5	4.1	18	3	US-08-881-094-3	Sequence 3, Appl1
156	6	5.0	832	2	US-08-599-491-4	Sequence 4, Appl1	229	5	4.1	18	3	US-08-881-094-9	Sequence 9, Appl1
157	6	5.0	832	2	US-08-756-386-4	Sequence 4, Appl1	230	5	4.1	18	3	US-08-881-094-10	Sequence 10, Appl
158	6	5.0	832	2	US-08-823-516-4	Sequence 4, Appl1	231	5	4.1	19	3	US-08-788-231A-14	Sequence 14, Appl
159	6	5.0	832	3	US-08-682-853A-4	Sequence 4, Appl1	232	5	4.1	20	3	US-08-399-696-79	Sequence 79, Appl
160	6	5.0	832	3	US-08-759-038-4	Sequence 4, Appl1	233	5	4.1	20	3	US-08-837-226-12	Sequence 12, Appl
161	6	5.0	832	3	US-08-758-314-4	Sequence 4, Appl1	234	5	4.1	21	1	US-08-706-344C-9	Sequence 9, Appl1
162	6	5.0	832	5	PCR-US91-07035-2	Sequence 2, Appl1	235	5	4.1	21	1	US-07-768-269-15	Sequence 15, Appl
163	6	5.0	833	1	US-08-073-384C-8	Sequence 8, Appl1	236	5	4.1	21	1	US-07-908-455A-6	Sequence 6, Appl1
164	6	5.0	833	1	US-08-254-359A-8	Sequence 8, Appl1	237	5	4.1	21	1	US-07-908-455A-7	Sequence 7, Appl1
165	6	5.0	833	1	US-08-483-043-8	Sequence 8, Appl1	238	5	4.1	21	1	US-08-434-120-32	Sequence 32, Appl
166	6	5.0	833	1	US-08-481-238-8	Sequence 8, Appl1	239	5	4.1	21	1	US-08-434-120-33	Sequence 33, Appl
167	6	5.0	833	2	US-08-471-066B-8	Sequence 8, Appl1	240	5	4.1	21	1	US-08-465-325-33	Sequence 33, Appl
168	6	5.0	833	2	US-08-484-956-8	Sequence 8, Appl1	241	5	4.1	21	1	US-08-465-325-33	Sequence 33, Appl
169	6	5.0	833	2	US-08-484-956-85	Sequence 85, Appl	242	5	4.1	21	4	US-08-635-928-24	Sequence 24, Appl
170	6	5.0	833	2	US-08-757-653-8	Sequence 8, Appl1	243	5	4.1	22	1	US-08-380-438-3	Sequence 3, Appl1
171	6	5.0	833	2	US-08-757-653-85	Sequence 85, Appl	244	5	4.1	22	2	US-08-169-948B-30	Sequence 30, Appl
172	6	5.0	833	2	US-08-757-653-168	Sequence 168, App	245	5	4.1	22	2	US-08-448-873-30	Sequence 30, Appl
173	6	5.0	833	2	US-08-757-653-188	Sequence 188, App	246	5	4.1	22	3	US-08-940-095-39	Sequence 39, Appl

247	5	4.1	22	3	US-08-940-095-57	Sequence 57, Appl	320	5	4.1	37	1	US-08-471-675A-25	Sequence 25, Appl
248	5	4.1	22	3	US-08-940-095-134	Sequence 134, Appl	321	5	4.1	37	1	US-08-471-675A-27	Sequence 27, Appl
249	5	4.1	22	3	US-08-940-093-39	Sequence 39, Appl	322	5	4.1	37	2	US-08-259-762-10	Sequence 10, Appl
250	5	4.1	22	3	US-08-940-093-57	Sequence 57, Appl	323	5	4.1	37	2	US-08-259-762-11	Sequence 11, Appl
251	5	4.1	22	3	US-08-940-093-134	Sequence 134, Appl	324	5	4.1	37	2	US-08-892-549-29	Sequence 29, Appl
252	5	4.1	22	3	US-08-940-096-39	Sequence 39, Appl	325	5	4.1	37	2	US-08-892-549-31	Sequence 31, Appl
253	5	4.1	22	3	US-08-940-096-57	Sequence 57, Appl	326	5	4.1	37	3	US-08-302-069A-24	Sequence 24, Appl
254	5	4.1	22	3	US-08-940-096-134	Sequence 134, Appl	327	5	4.1	37	3	US-08-302-069A-26	Sequence 26, Appl
255	5	4.1	22	4	US-09-465-719-39	Sequence 39, Appl	328	5	4.1	40	3	US-08-792-832A-54	Sequence 54, Appl
256	5	4.1	22	4	US-09-465-719-57	Sequence 57, Appl	329	5	4.1	40	3	US-08-792-832A-56	Sequence 56, Appl
257	5	4.1	22	4	US-09-465-719-134	Sequence 134, Appl	330	5	4.1	41	4	US-08-789-333F-27	Sequence 27, Appl
258	5	4.1	22	4	US-08-382-452D-30	Sequence 30, Appl	331	5	4.1	41	4	US-09-169-015-37	Sequence 37, Appl
259	5	4.1	22	4	US-08-112-208C-20	Sequence 20, Appl	332	5	4.1	41	4	US-09-133-944-26	Sequence 26, Appl
260	5	4.1	23	1	US-08-248-819A-22	Sequence 22, Appl	333	5	4.1	42	4	US-09-309-382-12	Sequence 12, Appl
261	5	4.1	23	2	US-08-337-646A-40	Sequence 40, Appl	334	5	4.1	47	2	US-08-935-396-2	Sequence 2, Appl
262	5	4.1	23	2	US-08-856-531-20	Sequence 20, Appl	335	5	4.1	47	2	US-08-935-396-2	Sequence 2, Appl
263	5	4.1	23	2	US-08-856-531-20	Sequence 20, Appl	336	5	4.1	51	1	US-08-346-849-12	Sequence 12, Appl
264	5	4.1	23	4	US-08-927-326-40	Sequence 40, Appl	337	5	4.1	51	2	US-08-293-284A-12	Sequence 12, Appl
265	5	4.1	24	1	US-08-325-071-30	Sequence 30, Appl	338	5	4.1	51	2	US-08-485-443B-39	Sequence 39, Appl
266	5	4.1	24	1	US-08-181-271A-52	Sequence 52, Appl	339	5	4.1	54	1	US-08-485-443B-39	Sequence 39, Appl
267	5	4.1	24	1	US-08-449-315-52	Sequence 52, Appl	340	5	4.1	54	2	US-08-482-130C-39	Sequence 39, Appl
268	5	4.1	24	1	US-08-449-315-52	Sequence 52, Appl	341	5	4.1	54	2	US-08-482-130C-39	Sequence 39, Appl
269	5	4.1	24	1	US-08-449-043-52	Sequence 52, Appl	342	5	4.1	54	3	US-08-484-211C-39	Sequence 39, Appl
270	5	4.1	24	1	US-08-456-265A-52	Sequence 52, Appl	343	5	4.1	54	3	US-08-906-769-39	Sequence 39, Appl
271	5	4.1	24	1	US-08-456-265A-52	Sequence 52, Appl	344	5	4.1	54	3	US-08-906-769-39	Sequence 39, Appl
272	5	4.1	24	1	US-08-455-244-52	Sequence 52, Appl	345	5	4.1	54	4	US-08-817-795-39	Sequence 39, Appl
273	5	4.1	24	1	US-08-454-876-52	Sequence 52, Appl	346	5	4.1	54	4	US-08-817-795-39	Sequence 39, Appl
274	5	4.1	24	2	US-08-457-364-52	Sequence 52, Appl	347	5	4.1	54	4	US-08-485-443B-39	Sequence 39, Appl
275	5	4.1	24	2	US-08-456-262-52	Sequence 52, Appl	348	5	4.1	54	4	US-08-639-075A-39	Sequence 39, Appl
276	5	4.1	24	2	US-08-456-240-52	Sequence 52, Appl	349	5	4.1	54	4	US-09-012-431-39	Sequence 39, Appl
277	5	4.1	24	2	US-08-455-736-52	Sequence 52, Appl	350	5	4.1	54	4	US-09-012-431-39	Sequence 39, Appl
278	5	4.1	24	2	US-08-971-217-52	Sequence 52, Appl	351	5	4.1	56	4	US-08-906-613-39	Sequence 39, Appl
279	5	4.1	24	4	US-08-461-004A-30	Sequence 30, Appl	352	5	4.1	56	4	US-08-906-613-39	Sequence 39, Appl
280	5	4.1	24	4	US-08-350-600-52	Sequence 52, Appl	353	5	4.1	56	4	US-08-906-613-39	Sequence 39, Appl
281	5	4.1	25	1	US-08-172-331B-9	Sequence 9, Appl	354	5	4.1	67	1	US-08-630-524-14	Sequence 14, Appl
282	5	4.1	25	1	US-08-468-709B-13	Sequence 13, Appl	355	5	4.1	67	1	US-07-938-782A-14	Sequence 14, Appl
283	5	4.1	25	1	US-08-468-709B-15	Sequence 15, Appl	356	5	4.1	67	1	US-08-248-839C-159	Sequence 159, Appl
284	5	4.1	25	1	US-08-468-709B-16	Sequence 16, Appl	357	5	4.1	75	2	US-08-903-223-330	Sequence 330, Appl
285	5	4.1	25	2	US-08-241-664B-13	Sequence 13, Appl	358	5	4.1	75	2	US-08-469-537A-38	Sequence 38, Appl
286	5	4.1	25	2	US-08-241-664B-13	Sequence 13, Appl	359	5	4.1	76	2	US-08-469-537A-39	Sequence 39, Appl
287	5	4.1	25	2	US-08-241-664B-15	Sequence 15, Appl	360	5	4.1	76	2	US-08-469-537A-40	Sequence 40, Appl
288	5	4.1	26	1	US-08-281-702A-6	Sequence 6, Appl	361	5	4.1	77	2	US-08-225-577B-13	Sequence 13, Appl
289	5	4.1	26	1	US-08-181-271A-53	Sequence 53, Appl	362	5	4.1	77	2	US-08-469-537A-41	Sequence 41, Appl
290	5	4.1	26	1	US-08-449-315-53	Sequence 53, Appl	363	5	4.1	79	4	US-08-469-537A-46	Sequence 46, Appl
291	5	4.1	26	1	US-08-449-315-53	Sequence 53, Appl	364	5	4.1	82	1	US-08-903-223-277	Sequence 277, Appl
292	5	4.1	26	1	US-08-449-043-53	Sequence 53, Appl	365	5	4.1	84	3	US-08-225-577B-12	Sequence 12, Appl
293	5	4.1	26	1	US-08-456-265A-53	Sequence 53, Appl	366	5	4.1	84	3	US-08-906-769-99	Sequence 99, Appl
294	5	4.1	26	1	US-08-455-416-53	Sequence 53, Appl	367	5	4.1	84	4	US-08-906-616-99	Sequence 99, Appl
295	5	4.1	26	1	US-08-455-244-53	Sequence 53, Appl	368	5	4.1	84	4	US-08-817-795-99	Sequence 99, Appl
296	5	4.1	26	1	US-08-454-876-53	Sequence 53, Appl	369	5	4.1	84	4	US-08-639-075A-99	Sequence 99, Appl
297	5	4.1	26	2	US-08-618-917-6	Sequence 6, Appl	370	5	4.1	84	4	US-08-012-431-99	Sequence 99, Appl
298	5	4.1	26	2	US-08-457-364-53	Sequence 53, Appl	371	5	4.1	84	4	US-08-012-431-99	Sequence 99, Appl
299	5	4.1	26	2	US-08-456-262-53	Sequence 53, Appl	372	5	4.1	84	5	US-08-906-613-99	Sequence 99, Appl
300	5	4.1	26	2	US-08-456-240-53	Sequence 53, Appl	373	5	4.1	88	2	PCT-US95-14442A-99	Sequence 99, Appl
301	5	4.1	26	2	US-08-455-736-53	Sequence 53, Appl	374	5	4.1	88	2	PCT-US95-14442A-99	Sequence 99, Appl
302	5	4.1	26	2	US-08-620-151-101	Sequence 101, Appl	375	5	4.1	90	1	US-08-690-011A-11	Sequence 11, Appl
303	5	4.1	26	2	US-08-971-217-53	Sequence 53, Appl	376	5	4.1	90	3	US-08-341-219-24	Sequence 24, Appl
304	5	4.1	26	2	US-08-389-564B-27	Sequence 27, Appl	377	5	4.1	90	3	US-08-173-581-4	Sequence 4, Appl
305	5	4.1	26	3	US-08-466-047B-27	Sequence 27, Appl	378	5	4.1	90	4	US-08-912-314A-24	Sequence 24, Appl
306	5	4.1	26	4	US-09-350-600-53	Sequence 53, Appl	379	5	4.1	92	1	US-08-341-219-21	Sequence 21, Appl
307	5	4.1	27	2	US-08-310-912A-201	Sequence 201, Appl	380	5	4.1	92	1	US-08-912-314A-21	Sequence 21, Appl
308	5	4.1	27	4	US-09-301-085-201	Sequence 201, Appl	381	5	4.1	96	2	US-08-739-484-4	Sequence 4, Appl
309	5	4.1	27	5	PCT-US95-04589-201	Sequence 201, Appl	382	5	4.1	96	4	US-08-465-343A-11	Sequence 11, Appl
310	5	4.1	31	2	US-08-231-472-9	Sequence 9, Appl	383	5	4.1	98	2	US-08-690-011A-19	Sequence 19, Appl
311	5	4.1	31	3	US-09-248-082-9	Sequence 9, Appl	384	5	4.1	100	1	US-08-967-513-3	Sequence 3, Appl
312	5	4.1	33	6	5169933-45	Patent No. 5169933	385	5	4.1	100	2	US-08-619-542B-35	Sequence 35, Appl
313	5	4.1	35	4	US-08-749-066A-6	Sequence 6, Appl	386	5	4.1	100	2	US-08-467-822-23	Sequence 23, Appl
314	5	4.1	36	1	US-07-929-206-7	Sequence 7, Appl	387	5	4.1	100	4	US-08-432-697-23	Sequence 23, Appl
315	5	4.1	36	2	US-08-313-185-4	Sequence 4, Appl	388	5	4.1	100	4	US-08-466-248-23	Sequence 23, Appl
316	5	4.1	36	2	US-08-459-499-7	Sequence 7, Appl	389	5	4.1	101	1	US-08-271-354-13	Sequence 13, Appl
317	5	4.1	36	3	US-08-082-614A-4	Sequence 4, Appl	390	5	4.1	101	2	US-08-565-861-13	Sequence 13, Appl
318	5	4.1	37	1	US-08-477-727A-103	Sequence 103, Appl	391	5	4.1	101	5	PCT-US94-07658-13	Sequence 13, Appl
319	5	4.1	37	1	US-08-477-727A-105	Sequence 105, Appl	392	5	4.1	102	3	US-08-906-769-125	Sequence 125, Appl

393	4.1	102	3	US-08-906-616-125	Sequence 125, App	466	5	4.1	160	1	US-07-847-010-11	Sequence 11, Appl
394	4.1	102	4	US-08-639-075A-125	Sequence 125, App	467	5	4.1	160	1	US-07-847-010-14	Sequence 17, Appl
395	4.1	102	4	US-09-012-431-125	Sequence 125, App	468	5	4.1	160	1	US-07-847-010-17	Sequence 17, Appl
396	4.1	102	4	US-09-012-692-125	Sequence 125, App	469	5	4.1	160	1	US-07-847-010-20	Sequence 20, Appl
397	4.1	102	4	US-08-906-613-125	Sequence 125, App	470	5	4.1	160	2	US-08-726-306A-35	Sequence 35, Appl
398	4.1	102	4	US-08-619-542B-38	Sequence 38, Appl	471	5	4.1	161	1	US-08-368-832-2	Sequence 2, Appl
399	4.1	103	3	US-08-894-173-76	Sequence 76, Appl	472	5	4.1	161	2	US-08-525-940-2	Sequence 2, Appl
400	4.1	103	3	US-09-398-193-76	Sequence 76, Appl	473	5	4.1	161	2	US-08-976-838-2	Sequence 2, Appl
401	4.1	103	4	US-08-857-076-54	Sequence 54, Appl	474	5	4.1	161	3	US-09-205-264-2	Sequence 2, Appl
402	4.1	105	2	US-08-646-981-3	Sequence 3, Appl	475	5	4.1	162	1	US-07-879-685B-4	Sequence 4, Appl
403	4.1	106	3	US-09-083-351-16	Sequence 16, Appl	476	5	4.1	162	4	US-09-108-020-50	Sequence 50, Appl
404	4.1	106	3	US-09-083-351-17	Sequence 17, Appl	477	5	4.1	165	1	US-08-051-142-2	Sequence 2, Appl
405	4.1	106	3	US-09-083-351-18	Sequence 18, Appl	478	5	4.1	165	2	US-08-602-208-3	Sequence 3, Appl
406	4.1	106	4	US-09-083-352-16	Sequence 16, Appl	479	5	4.1	172	2	US-08-853-659A-46	Sequence 46, Appl
407	4.1	106	4	US-09-083-352-17	Sequence 17, Appl	480	5	4.1	175	1	US-08-010-099-94	Sequence 94, Appl
408	4.1	106	4	US-09-083-352-18	Sequence 18, Appl	481	5	4.1	175	4	US-08-448-716-94	Sequence 94, Appl
409	4.1	106	4	US-08-857-076-37	Sequence 37, Appl	482	5	4.1	175	4	US-09-304-186-94	Sequence 94, Appl
410	4.1	107	2	US-08-810-572A-4	Sequence 4, Appl	483	5	4.1	178	1	US-08-673-269-2	Sequence 2, Appl
411	4.1	108	2	US-08-828-233-3	Sequence 3, Appl	484	5	4.1	179	1	US-08-607-269-27	Sequence 27, Appl
412	4.1	108	2	US-08-828-233-4	Sequence 4, Appl	485	5	4.1	179	5	PCT-US95-04600-27	Sequence 27, Appl
413	4.1	108	3	US-09-205-679-3	Sequence 3, Appl	486	5	4.1	181	1	US-08-471-058-18	Sequence 18, Appl
414	4.1	108	3	US-09-205-679-4	Sequence 4, Appl	487	5	4.1	181	3	US-08-471-057-18	Sequence 18, Appl
415	4.1	109	1	US-08-466-886-24	Sequence 24, Appl	488	5	4.1	188	2	US-08-726-306A-57	Sequence 57, Appl
416	4.1	109	2	US-08-637-759B-261	Sequence 261, App	489	5	4.1	189	1	US-08-152-485-4	Sequence 4, Appl
417	4.1	109	3	US-08-871-355A-261	Sequence 261, App	490	5	4.1	189	1	US-08-463-089-4	Sequence 4, Appl
418	4.1	109	3	US-08-894-173-96	Sequence 96, Appl	491	5	4.1	189	1	US-08-461-360A-4	Sequence 4, Appl
419	4.1	109	4	US-09-398-193-96	Sequence 96, Appl	492	5	4.1	189	5	US-08-461-360A-4	Sequence 4, Appl
420	4.1	109	4	US-08-469-617-24	Sequence 24, Appl	493	5	4.1	189	5	PCT-US94-12904-4	Sequence 4, Appl
421	4.1	109	4	US-08-857-076-56	Sequence 56, Appl	494	5	4.1	193	2	US-08-308-821A-6	Sequence 6, Appl
422	4.1	109	5	PCT-US95-09589-2	Sequence 2, Appl	495	5	4.1	193	3	US-08-831-627-6	Sequence 6, Appl
423	4.1	109	5	US-08-516-859A-2	Sequence 2, Appl	496	5	4.1	193	3	US-08-765-381-15	Sequence 15, Appl
424	4.1	110	3	US-08-516-859A-101	Sequence 101, App	497	5	4.1	193	3	US-08-881-094-17	Sequence 17, Appl
425	4.1	112	2	US-08-739-484-3	Sequence 3, Appl	498	5	4.1	197	4	US-08-804-372A-32	Sequence 32, Appl
426	4.1	114	2	US-08-828-239-1	Sequence 1, Appl	499	5	4.1	200	1	US-07-855-412B-1	Sequence 1, Appl
427	4.1	114	2	US-09-205-679-1	Sequence 1, Appl	500	5	4.1	200	2	US-08-308-887A-1	Sequence 1, Appl
428	4.1	116	2	US-08-846-134-1	Sequence 1, Appl	501	5	4.1	200	3	US-08-881-094-1	Sequence 1, Appl
429	4.1	116	2	US-08-853-659A-42	Sequence 42, Appl	502	5	4.1	201	1	US-08-236-427-3	Sequence 3, Appl
430	4.1	117	3	US-08-234-812-1	Sequence 1, Appl	503	5	4.1	201	4	US-09-220-528-116	Sequence 116, App
431	4.1	117	3	US-08-545-809A-133	Sequence 133, App	504	5	4.1	202	3	US-08-881-094-16	Sequence 18, Appl
432	4.1	117	4	US-09-036-315-6	Sequence 6, Appl	505	5	4.1	202	3	US-08-852-936C-4	Sequence 4, Appl
433	4.1	118	2	US-08-663-809-1	Sequence 1, Appl	506	5	4.1	203	4	US-09-300-328-4	Sequence 4, Appl
434	4.1	118	5	PCT-US93-08435-10	Sequence 10, Appl	507	5	4.1	204	3	US-09-053-197A-29	Sequence 29, Appl
435	4.1	120	1	US-08-542-363-26	Sequence 26, Appl	508	5	4.1	205	1	US-08-155-171B-17	Sequence 17, Appl
436	4.1	120	4	US-09-100-089-26	Sequence 26, Appl	509	5	4.1	205	2	US-08-435-998-17	Sequence 17, Appl
437	4.1	122	1	US-08-266-451B-18	Sequence 18, Appl	510	5	4.1	207	1	US-08-557-917A-2	Sequence 2, Appl
438	4.1	122	2	US-08-748-725-18	Sequence 18, Appl	511	5	4.1	207	4	US-09-084-153-2	Sequence 2, Appl
439	4.1	123	4	US-09-188-930-292	Sequence 292, App	512	5	4.1	207	4	US-08-309-512-4	Sequence 2, Appl
440	4.1	126	6	5268359-5	Patent No. 5268359	513	5	4.1	208	1	US-08-084-079-2	Sequence 4, Appl
441	4.1	127	2	US-08-637-759B-334	Sequence 334, App	514	5	4.1	208	5	PCT-US92-08756A-4	Sequence 4, Appl
442	4.1	127	3	US-08-871-355A-334	Sequence 334, App	515	5	4.1	210	1	US-07-667-276A-2	Sequence 2, Appl
443	4.1	130	6	5268359-2	Patent No. 5268359	516	5	4.1	210	4	US-08-617-785-16	Sequence 16, Appl
444	4.1	137	1	US-08-468-709B-4	Sequence 4, Appl	517	5	4.1	214	1	US-08-155-171B-16	Sequence 16, Appl
445	4.1	137	1	US-08-468-709B-11	Sequence 11, Appl	518	5	4.1	214	2	US-08-435-998-16	Sequence 16, Appl
446	4.1	137	2	US-08-241-664B-4	Sequence 4, Appl	519	5	4.1	216	3	US-08-506-553C-23	Sequence 23, Appl
447	4.1	137	2	US-08-241-664B-11	Sequence 11, Appl	520	5	4.1	219	1	US-08-470-261-2	Sequence 2, Appl
448	4.1	137	4	US-09-383-586-37	Sequence 37, Appl	521	5	4.1	219	3	US-08-916-989B-2	Sequence 2, Appl
449	4.1	137	4	PCT-US93-03936-4	Sequence 4, Appl	522	5	4.1	219	5	PCT-US94-13187-2	Sequence 2, Appl
450	4.1	144	4	US-09-319-989-4	Sequence 4, Appl	523	5	4.1	220	4	US-08-297-431B-31	Sequence 31, Appl
451	4.1	146	4	US-08-792-013-7	Sequence 7, Appl	524	5	4.1	220	4	US-08-884-077-2	Sequence 2, Appl
452	4.1	147	1	US-08-171-385-5	Sequence 5, Appl	525	5	4.1	221	4	US-08-297-431B-2	Sequence 2, Appl
453	4.1	147	2	US-08-949-584A-2	Sequence 2, Appl	526	5	4.1	221	4	US-08-297-431B-4	Sequence 4, Appl
454	4.1	147	3	US-08-946-329A-59	Sequence 59, Appl	527	5	4.1	221	4	US-08-297-431B-6	Sequence 6, Appl
455	4.1	147	3	US-08-361-441B-5	Sequence 5, Appl	528	5	4.1	221	4	US-08-297-431B-8	Sequence 8, Appl
456	4.1	147	3	US-08-361-441B-42	Sequence 42, Appl	529	5	4.1	221	4	US-08-297-431B-10	Sequence 10, Appl
457	4.1	147	3	US-09-049-672A-27	Sequence 27, Appl	530	5	4.1	221	4	US-08-297-431B-12	Sequence 12, Appl
458	4.1	147	4	US-08-792-013-6	Sequence 4, Appl	531	5	4.1	221	4	US-08-297-431B-14	Sequence 14, Appl
459	4.1	147	4	US-08-792-013-4	Sequence 6, Appl	532	5	4.1	221	4	US-08-297-431B-16	Sequence 16, Appl
460	4.1	147	4	US-09-239-861-2	Sequence 2, Appl	533	5	4.1	221	4	US-08-297-431B-18	Sequence 18, Appl
461	4.1	150	4	US-09-049-672A-3	Sequence 3, Appl	534	5	4.1	221	4	US-08-297-431B-20	Sequence 20, Appl
462	4.1	154	2	US-08-756-749C-3	Sequence 3, Appl	535	5	4.1	221	4	US-08-297-431B-32	Sequence 32, Appl
463	4.1	156	2	US-08-777-321A-3	Sequence 3, Appl	536	5	4.1	222	2	US-08-756-771-3	Sequence 3, Appl
464	4.1	158	1	US-08-229-393-2	Sequence 2, Appl	537	5	4.1	222	2	US-08-756-771-4	Sequence 4, Appl
465	4.1	160	1	US-07-847-010-3	Sequence 3, Appl	538	5	4.1	222	2	US-08-446-875-14	Sequence 14, Appl

539	5	4.1	222	2	US-09-096-571-3	Sequence 3, Appl	612	5	4.1	274	2	US-08-701-191A-33	Sequence 33, Appl
540	5	4.1	222	2	US-09-096-571-4	Sequence 4, Appl	613	5	4.1	275	2	US-08-701-191A-38	Sequence 38, Appl
541	5	4.1	222	4	US-09-309-320-3	Sequence 3, Appl	614	5	4.1	275	2	US-07-857-224B-71	Sequence 71, Appl
542	5	4.1	222	4	US-09-309-320-4	Sequence 4, Appl	615	5	4.1	276	2	US-08-751-233A-4	Sequence 4, Appl
543	5	4.1	223	1	US-08-430-633-1	Sequence 1, Appl	616	5	4.1	276	3	US-08-506-553C-26	Sequence 26, Appl
544	5	4.1	223	2	US-08-936-854-1	Sequence 1, Appl	617	5	4.1	277	5	PCT-US96-10521-8	Sequence 8, Appl
545	5	4.1	225	1	US-08-360-657-8	Sequence 8, Appl	618	5	4.1	278	1	US-08-258-261B-20	Sequence 20, Appl
546	5	4.1	226	3	US-09-176-673-3	Sequence 3, Appl	619	5	4.1	278	1	US-08-456-837-20	Sequence 20, Appl
547	5	4.1	227	1	US-08-679-493A-23	Sequence 23, Appl	620	5	4.1	278	1	US-08-457-342-20	Sequence 20, Appl
548	5	4.1	227	1	US-08-360-103A-2	Sequence 2, Appl	621	5	4.1	278	1	US-08-457-646A-20	Sequence 20, Appl
549	5	4.1	231	1	US-08-287-959-7	Sequence 7, Appl	622	5	4.1	278	1	US-08-458-076A-20	Sequence 20, Appl
550	5	4.1	231	4	US-09-370-098-4	Sequence 4, Appl	623	5	4.1	278	1	US-08-457-335A-20	Sequence 20, Appl
551	5	4.1	233	4	US-08-438-745-15	Sequence 15, Appl	624	5	4.1	278	1	US-08-729-214-20	Sequence 20, Appl
552	5	4.1	233	4	US-08-438-745-17	Sequence 17, Appl	625	5	4.1	278	3	US-09-028-934-20	Sequence 20, Appl
553	5	4.1	233	4	US-09-219-019-15	Sequence 15, Appl	626	5	4.1	278	4	US-09-060-410-17	Sequence 17, Appl
554	5	4.1	233	4	US-09-219-019-17	Sequence 17, Appl	627	5	4.1	278	4	US-08-557-614-2	Sequence 2, Appl
555	5	4.1	233	5	PCT-US94-05669A-15	Sequence 15, Appl	628	5	4.1	278	4	US-08-557-614-23	Sequence 23, Appl
556	5	4.1	233	5	PCT-US94-05669A-17	Sequence 17, Appl	629	5	4.1	280	4	US-09-383-586-18	Sequence 18, Appl
557	5	4.1	235	4	US-08-438-745-13	Sequence 13, Appl	630	5	4.1	283	4	US-09-135-021-6	Sequence 6, Appl
558	5	4.1	235	4	US-09-219-019-13	Sequence 13, Appl	631	5	4.1	284	2	US-08-751-233A-6	Sequence 6, Appl
559	5	4.1	235	4	US-09-244-314-4	Sequence 4, Appl	632	5	4.1	284	2	US-08-751-233A-8	Sequence 8, Appl
560	5	4.1	235	5	PCT-US94-05669A-13	Sequence 13, Appl	633	5	4.1	291	2	US-08-688-342-5	Sequence 5, Appl
561	5	4.1	235	5	PCT-US96-10521-5	Sequence 5, Appl	634	5	4.1	291	2	US-09-113-788-5	Sequence 5, Appl
562	5	4.1	246	1	US-07-887-072B-4	Sequence 4, Appl	635	5	4.1	291	4	US-09-328-869-2	Sequence 2, Appl
563	5	4.1	246	1	US-08-466-444-4	Sequence 4, Appl	636	5	4.1	291	4	US-09-105-697-4	Sequence 4, Appl
564	5	4.1	249	2	US-08-685-992-29	Sequence 29, Appl	637	5	4.1	291	4	US-09-105-697-6	Sequence 6, Appl
565	5	4.1	249	2	US-09-144-925-29	Sequence 29, Appl	638	5	4.1	291	4	US-09-105-697-6	Sequence 6, Appl
566	5	4.1	252	1	US-07-717-332D-2	Sequence 2, Appl	639	5	4.1	291	4	US-09-111-470-5	Sequence 5, Appl
567	5	4.1	252	1	US-08-411-777-8	Sequence 8, Appl	640	5	4.1	291	4	US-09-629-774A-2	Sequence 2, Appl
568	5	4.1	252	2	US-08-853-659A-43	Sequence 43, Appl	641	5	4.1	292	1	US-08-701-191A-26	Sequence 26, Appl
569	5	4.1	252	3	US-09-057-088-8	Sequence 8, Appl	642	5	4.1	292	2	US-08-610-572A-2	Sequence 2, Appl
570	5	4.1	255	5	PCT-US96-01314-54	Sequence 54, Appl	643	5	4.1	292	2	US-08-688-342-4	Sequence 4, Appl
571	5	4.1	256	3	US-09-035-706-4	Sequence 4, Appl	644	5	4.1	292	3	US-09-113-788-4	Sequence 4, Appl
572	5	4.1	256	3	US-08-955-841-4	Sequence 4, Appl	645	5	4.1	292	3	US-08-994-570-3	Sequence 3, Appl
573	5	4.1	256	5	PCT-US96-01314-55	Sequence 55, Appl	646	5	4.1	293	2	US-08-701-191A-26	Sequence 26, Appl
574	5	4.1	257	1	US-08-618-164-2	Sequence 2, Appl	647	5	4.1	293	3	US-09-276-873-2	Sequence 2, Appl
575	5	4.1	258	3	US-07-857-224B-5	Sequence 3, Appl	648	5	4.1	293	4	US-08-438-745-4	Sequence 4, Appl
576	5	4.1	258	3	US-09-035-706-3	Sequence 3, Appl	649	5	4.1	293	4	US-08-438-745-6	Sequence 6, Appl
577	5	4.1	258	3	US-08-955-841-3	Sequence 3, Appl	650	5	4.1	293	4	US-09-219-019-4	Sequence 4, Appl
578	5	4.1	259	2	US-07-857-224B-49	Sequence 49, Appl	651	5	4.1	293	4	US-09-219-019-6	Sequence 6, Appl
579	5	4.1	259	2	US-07-857-224B-50	Sequence 50, Appl	652	5	4.1	293	5	PCT-US94-05669A-4	Sequence 4, Appl
580	5	4.1	259	2	US-07-857-224B-51	Sequence 51, Appl	653	5	4.1	293	5	PCT-US94-05669A-6	Sequence 6, Appl
581	5	4.1	259	2	US-07-857-224B-52	Sequence 52, Appl	654	5	4.1	294	4	US-09-518-046-4	Sequence 4, Appl
582	5	4.1	259	2	US-07-857-224B-54	Sequence 54, Appl	655	5	4.1	299	4	US-09-352-990-22	Sequence 22, Appl
583	5	4.1	259	2	US-07-857-224B-55	Sequence 55, Appl	656	5	4.1	300	1	US-07-640-029-5	Sequence 5, Appl
584	5	4.1	259	2	US-07-857-224B-56	Sequence 56, Appl	657	5	4.1	300	2	US-08-487-031-2	Sequence 2, Appl
585	5	4.1	260	2	US-07-857-224B-6	Sequence 6, Appl	658	5	4.1	300	3	US-08-473-034-2	Sequence 2, Appl
586	5	4.1	260	5	PCT-US96-03916-9	Sequence 9, Appl	659	5	4.1	300	4	US-08-439-992A-5	Sequence 5, Appl
587	5	4.1	260	5	US-07-857-224B-70	Sequence 70, Appl	660	5	4.1	302	1	US-07-640-029-6	Sequence 6, Appl
588	5	4.1	261	2	US-07-857-224B-22	Sequence 22, Appl	661	5	4.1	302	1	US-07-921-807B-7	Sequence 7, Appl
589	5	4.1	261	3	US-09-329-418-6	Sequence 6, Appl	662	5	4.1	302	1	US-07-921-807B-8	Sequence 8, Appl
590	5	4.1	261	4	US-09-531-914-6	Sequence 6, Appl	663	5	4.1	302	1	US-08-441-944A-7	Sequence 7, Appl
591	5	4.1	262	1	US-08-397-633A-73	Sequence 73, Appl	664	5	4.1	302	1	US-08-441-944A-8	Sequence 8, Appl
592	5	4.1	262	2	US-07-857-224B-57	Sequence 57, Appl	665	5	4.1	302	4	US-08-439-992A-6	Sequence 6, Appl
593	5	4.1	262	2	US-07-857-224B-62	Sequence 62, Appl	666	5	4.1	304	2	US-08-487-031-5	Sequence 5, Appl
594	5	4.1	262	2	US-07-857-224B-63	Sequence 63, Appl	667	5	4.1	304	3	US-08-473-034-5	Sequence 5, Appl
595	5	4.1	262	2	US-07-857-224B-64	Sequence 64, Appl	668	5	4.1	305	2	US-08-853-659A-47	Sequence 47, Appl
596	5	4.1	262	4	US-09-363-189B-6	Sequence 6, Appl	669	5	4.1	306	1	US-08-368-852-13	Sequence 13, Appl
597	5	4.1	264	2	US-07-857-224B-34	Sequence 34, Appl	670	5	4.1	306	2	US-08-525-940-13	Sequence 13, Appl
598	5	4.1	264	3	US-08-969-644-12	Sequence 12, Appl	671	5	4.1	306	2	US-08-976-838-13	Sequence 13, Appl
599	5	4.1	264	3	US-08-444-189-12	Sequence 12, Appl	672	5	4.1	307	4	US-09-049-672A-9	Sequence 9, Appl
600	5	4.1	264	4	US-08-465-455-2	Sequence 2, Appl	673	5	4.1	309	2	US-08-701-191A-9	Sequence 9, Appl
601	5	4.1	264	4	US-08-468-544-12	Sequence 12, Appl	674	5	4.1	312	3	US-08-258-287B-55	Sequence 55, Appl
602	5	4.1	268	1	US-08-015-973-7	Sequence 7, Appl	675	5	4.1	312	3	US-08-368-704C-53	Sequence 53, Appl
603	5	4.1	268	2	US-08-448-164-7	Sequence 7, Appl	676	5	4.1	312	4	US-08-460-900C-14	Sequence 14, Appl
604	5	4.1	268	4	US-08-081-929-7	Sequence 7, Appl	677	5	4.1	312	4	US-08-674-509B-14	Sequence 14, Appl
605	5	4.1	269	2	US-08-701-191A-35	Sequence 35, Appl	678	5	4.1	312	4	US-08-954-698-14	Sequence 14, Appl
606	5	4.1	270	2	US-07-857-224B-76	Sequence 76, Appl	679	5	4.1	313	2	US-08-356-060A-14	Sequence 14, Appl
607	5	4.1	271	2	US-07-857-224B-46	Sequence 46, Appl	680	5	4.1	313	2	US-08-446-806-1	Sequence 1, Appl
608	5	4.1	271	6	5175255-1	Patent No. 5175255	681	5	4.1	314	4	US-09-385-028-6	Sequence 6, Appl
609	5	4.1	273	2	US-08-701-191A-32	Sequence 32, Appl	682	5	4.1	316	4	US-09-111-470-4	Sequence 4, Appl
610	5	4.1	274	2	US-08-469-537A-55	Sequence 55, Appl	683	5	4.1	322	2	US-08-353-476-63	Sequence 63, Appl
611	5	4.1	274	2			684	5	4.1	323	1	US-07-913-107-2	Sequence 2, Appl

685	5	4.1	323	1	US-08-459-201-2	Sequence 2, Appl	758	5	4.1	361	1	US-08-458-076A-3	Sequence 3, Appl
686	5	4.1	323	1	US-08-281-248-2	Sequence 2, Appl	759	5	4.1	361	1	US-08-457-335A-3	Sequence 3, Appl
687	5	4.1	323	1	US-08-838-543-4	Sequence 4, Appl	760	5	4.1	361	1	US-08-729-214-3	Sequence 3, Appl
688	5	4.1	323	5	PCT-US93-06421-1	Sequence 1, Appl	761	5	4.1	361	3	US-09-028-934-3	Sequence 3, Appl
689	5	4.1	325	2	US-08-353-476-64	Sequence 64, Appl	762	5	4.1	361	3	US-09-108-020-47	Sequence 47, Appl
690	5	4.1	325	4	US-09-108-020-49	Sequence 49, Appl	763	5	4.1	363	1	US-07-681-704A-2	Sequence 2, Appl
691	5	4.1	325	4	US-09-041-886-33	Sequence 33, Appl	764	5	4.1	363	3	US-09-068-109-2	Sequence 2, Appl
692	5	4.1	327	3	US-08-513-974B-372	Sequence 372, App	765	5	4.1	363	3	US-09-082-089-5	Sequence 5, Appl
693	5	4.1	328	3	US-08-513-974B-39	Sequence 39, Appl	766	5	4.1	363	4	US-09-108-020-44	Sequence 44, Appl
694	5	4.1	328	3	US-08-513-974B-371	Sequence 371, App	767	5	4.1	366	3	US-09-176-657-2	Sequence 2, Appl
695	5	4.1	329	1	US-08-225-477B-3	Sequence 3, Appl	768	5	4.1	366	3	US-08-746-883-6	Sequence 6, Appl
696	5	4.1	329	5	PCT-US95-04353-3	Sequence 3, Appl	769	5	4.1	366	4	US-09-108-020-46	Sequence 46, Appl
697	5	4.1	330	1	US-08-118-270-21	Sequence 21, Appl	770	5	4.1	367	2	US-08-896-320-1	Sequence 1, Appl
698	5	4.1	330	2	US-08-487-031-10	Sequence 10, Appl	771	5	4.1	367	2	US-08-896-320-3	Sequence 3, Appl
699	5	4.1	330	3	US-08-473-034-10	Sequence 10, Appl	772	5	4.1	368	2	US-08-896-320-4	Sequence 4, Appl
700	5	4.1	330	4	US-09-145-391-2	Sequence 2, Appl	773	5	4.1	368	2	US-08-651-579-2	Sequence 2, Appl
701	5	4.1	330	5	PCT-US93-08528-21	Sequence 21, Appl	774	5	4.1	370	2	US-08-837-593-7	Sequence 7, Appl
702	5	4.1	331	2	US-08-646-981-17	Sequence 17, Appl	775	5	4.1	370	3	US-09-251-373-2	Sequence 2, Appl
703	5	4.1	331	3	US-09-037-190-49	Sequence 49, Appl	776	5	4.1	370	3	US-08-969-644-23	Sequence 23, Appl
704	5	4.1	331	3	US-09-037-192-49	Sequence 49, Appl	777	5	4.1	370	3	US-08-444-189-23	Sequence 23, Appl
705	5	4.1	331	4	US-09-049-691-49	Sequence 49, Appl	778	5	4.1	370	3	US-09-028-934-34	Sequence 34, Appl
706	5	4.1	332	4	US-09-037-143-49	Sequence 49, Appl	779	5	4.1	370	4	US-08-468-544-23	Sequence 23, Appl
707	5	4.1	332	4	US-08-260-174-49	Sequence 49, Appl	780	5	4.1	371	2	US-08-837-593-8	Sequence 8, Appl
708	5	4.1	333	1	US-08-436-044-4	Sequence 4, Appl	781	5	4.1	372	1	US-08-403-634-2	Sequence 2, Appl
709	5	4.1	333	2	US-08-436-054-4	Sequence 4, Appl	782	5	4.1	372	1	US-08-403-634-30	Sequence 30, Appl
710	5	4.1	333	4	US-08-271-948-2	Sequence 2, Appl	783	5	4.1	372	3	US-09-082-089-2	Sequence 2, Appl
711	5	4.1	333	5	PCT-US95-08534-2	Sequence 2, Appl	784	5	4.1	372	4	US-08-913-441B-2	Sequence 2, Appl
712	5	4.1	333	5	PCT-US95-08812-4	Sequence 4, Appl	785	5	4.1	372	4	US-08-913-441B-30	Sequence 30, Appl
713	5	4.1	334	2	US-08-665-647-3	Sequence 3, Appl	786	5	4.1	372	4	US-08-430-286A-6	Sequence 6, Appl
714	5	4.1	336	1	US-08-436-044-2	Sequence 2, Appl	787	5	4.1	375	1	US-08-464-523B-22	Sequence 22, Appl
715	5	4.1	336	2	US-08-784-651-4	Sequence 4, Appl	788	5	4.1	375	2	US-08-446-875-8	Sequence 8, Appl
716	5	4.1	336	2	US-08-436-054-2	Sequence 2, Appl	789	5	4.1	375	2	US-08-102-385G-8	Sequence 8, Appl
717	5	4.1	336	5	PCT-US95-08812-2	Sequence 2, Appl	790	5	4.1	376	2	US-08-875-972-2	Sequence 2, Appl
718	5	4.1	338	4	US-09-188-930-325	Sequence 325, App	791	5	4.1	377	1	US-07-772-087-2	Sequence 2, Appl
719	5	4.1	338	4	US-09-330-611-6	Sequence 6, Appl	792	5	4.1	378	3	US-09-057-969-6	Sequence 6, Appl
720	5	4.1	339	3	US-09-002-298-8	Sequence 8, Appl	793	5	4.1	378	4	US-09-082-088-2	Sequence 2, Appl
721	5	4.1	340	2	US-08-355-844-1	Sequence 1, Appl	794	5	4.1	381	2	US-08-867-057-3	Sequence 3, Appl
722	5	4.1	340	4	US-09-095-855-205	Sequence 205, App	795	5	4.1	381	2	US-09-128-369-3	Sequence 3, Appl
723	5	4.1	340	5	PCT-US95-16126-1	Sequence 1, Appl	796	5	4.1	383	5	PCT-US94-01321-2	Sequence 2, Appl
724	5	4.1	342	1	US-09-455-921A-2	Sequence 2, Appl	797	5	4.1	384	3	US-08-852-824-4	Sequence 4, Appl
725	5	4.1	343	1	US-08-463-090B-11	Sequence 11, Appl	798	5	4.1	384	3	US-09-209-668-15	Sequence 15, Appl
726	5	4.1	343	3	US-09-109-204-32	Sequence 32, Appl	799	5	4.1	384	4	US-09-025-580-33	Sequence 33, Appl
727	5	4.1	344	4	US-09-393-554-1	Sequence 1, Appl	800	5	4.1	384	4	US-09-025-580-35	Sequence 35, Appl
728	5	4.1	344	4	US-08-681-192-2	Sequence 2, Appl	801	5	4.1	384	5	PCT-US94-08119-12	Sequence 12, Appl
729	5	4.1	345	3	US-09-059-522-5	Sequence 5, Appl	802	5	4.1	385	1	PCT-US94-12919A-12	Sequence 12, Appl
730	5	4.1	345	4	US-09-382-027-5	Sequence 5, Appl	803	5	4.1	385	1	US-08-178-606-2	Sequence 2, Appl
731	5	4.1	346	1	US-08-213-403-2	Sequence 2, Appl	804	5	4.1	385	1	US-08-178-606-4	Sequence 4, Appl
732	5	4.1	346	1	US-08-458-077-2	Sequence 2, Appl	805	5	4.1	385	1	US-08-597-545-1	Sequence 1, Appl
733	5	4.1	346	1	US-08-460-741-2	Sequence 2, Appl	806	5	4.1	385	1	US-08-457-135-1	Sequence 1, Appl
734	5	4.1	346	1	US-08-747-240-2	Sequence 2, Appl	807	5	4.1	386	1	US-08-134-012-3	Sequence 3, Appl
735	5	4.1	346	1	US-08-299-567-6	Sequence 6, Appl	808	5	4.1	386	1	US-08-520-519-3	Sequence 3, Appl
736	5	4.1	346	3	US-09-173-581-3	Sequence 3, Appl	809	5	4.1	386	2	US-08-244-205-2	Sequence 2, Appl
737	5	4.1	346	4	US-08-915-498B-34	Sequence 34, Appl	810	5	4.1	386	5	PCT-US92-10284-2	Sequence 2, Appl
738	5	4.1	346	4	US-09-420-915-3	Sequence 3, Appl	811	5	4.1	388	2	US-08-282-197C-56	Sequence 56, Appl
739	5	4.1	348	1	US-08-229-781-50	Sequence 50, Appl	812	5	4.1	390	4	US-09-414-010-2	Sequence 2, Appl
740	5	4.1	348	1	US-08-630-918-50	Sequence 50, Appl	813	5	4.1	391	2	US-08-244-951A-10	Sequence 10, Appl
741	5	4.1	349	2	US-08-462-467B-18	Sequence 18, Appl	814	5	4.1	391	2	US-08-389-011-23	Sequence 23, Appl
742	5	4.1	350	2	US-08-468-790-2	Sequence 2, Appl	815	5	4.1	391	2	US-08-353-476-114	Sequence 114, App
743	5	4.1	350	4	US-09-157-603-3	Sequence 3, Appl	816	5	4.1	391	2	US-08-353-476-115	Sequence 115, App
744	5	4.1	350	4	US-09-587-436-3	Sequence 3, Appl	817	5	4.1	391	3	US-08-403-917A-23	Sequence 23, Appl
745	5	4.1	351	1	US-08-159-969-2	Sequence 2, Appl	818	5	4.1	391	4	US-09-348-952A-23	Sequence 23, Appl
746	5	4.1	351	2	US-08-468-012A-2	Sequence 2, Appl	819	5	4.1	392	2	US-08-886-152-1	Sequence 1, Appl
747	5	4.1	351	4	US-09-054-989-2	Sequence 2, Appl	820	5	4.1	392	2	US-08-886-152-3	Sequence 3, Appl
748	5	4.1	351	5	PCT-US93-05703-2	Sequence 2, Appl	821	5	4.1	392	4	US-09-026-408-2	Sequence 2, Appl
749	5	4.1	352	2	US-08-726-306A-17	Sequence 17, Appl	822	5	4.1	395	1	US-08-318-947A-18	Sequence 18, Appl
750	5	4.1	355	1	US-08-008-688A-2	Sequence 2, Appl	823	5	4.1	395	2	US-08-795-303-18	Sequence 18, Appl
751	5	4.1	359	2	US-08-812-203-3	Sequence 3, Appl	824	5	4.1	396	1	US-08-769-309A-15	Sequence 15, Appl
752	5	4.1	359	3	US-09-082-089-3	Sequence 3, Appl	825	5	4.1	396	3	US-08-994-570-15	Sequence 15, Appl
753	5	4.1	359	4	US-09-300-864-3	Sequence 3, Appl	826	5	4.1	397	3	US-08-989-478-14	Sequence 14, Appl
754	5	4.1	361	1	US-08-258-261B-3	Sequence 3, Appl	827	5	4.1	397	3	US-08-996-685-14	Sequence 14, Appl
755	5	4.1	361	1	US-08-456-837-3	Sequence 3, Appl	828	5	4.1	398	2	US-08-853-659A-45	Sequence 45, Appl
756	5	4.1	361	1	US-08-457-342-3	Sequence 3, Appl	829	5	4.1	399	6	5474928-2	Patent No. 5474928
757	5	4.1	361	1	US-08-457-646A-3	Sequence 3, Appl	830	5	4.1	400	3	US-08-938-830-29	Sequence 29, Appl

831	5	4.1	400	4	US-09-184-001-4	Sequence 4, Appli	904	419	4	US-08-640-906-2	Sequence 2, Appli
832	5	4.1	401	2	US-08-805-118-1	Sequence 1, Appli	905	419	4	US-08-640-906-17	Sequence 17, Appli
833	5	4.1	401	3	US-08-289-222E-3	Sequence 3, Appli	906	419	5	PCT-US92-10242-1	Sequence 1, Appli
834	5	4.1	401	4	US-09-054-526B-3	Sequence 3, Appli	907	420	5	US-08-588-258B-40	Sequence 40, Appli
835	5	4.1	403	2	US-08-533-669A-10	Sequence 10, Appli	908	420	3	US-08-846-762-73	Sequence 73, Appli
836	5	4.1	403	2	US-08-607-509-2	Sequence 2, Appli	909	420	3	US-09-329-418-8	Sequence 8, Appli
837	5	4.1	403	2	US-08-607-509-4	Sequence 4, Appli	910	420	5	US-09-531-914-8	Sequence 8, Appli
838	5	4.1	403	2	US-08-454-036-2	Sequence 2, Appli	911	420	5	PCT-US96-08295-40	Sequence 40, Appli
839	5	4.1	403	2	US-08-634-642-2	Sequence 2, Appli	912	421	2	US-08-353-476-113	Sequence 113, Appli
840	5	4.1	403	2	US-08-634-642-4	Sequence 4, Appli	913	421	2	US-08-494-907-14	Sequence 14, Appli
841	5	4.1	403	2	US-09-092-770-4	Sequence 4, Appli	914	423	2	US-08-846-762-74	Sequence 74, Appli
842	5	4.1	403	3	US-08-989-370-2	Sequence 2, Appli	915	423	4	US-09-243-374-6	Sequence 6, Appli
843	5	4.1	403	3	US-08-989-370-4	Sequence 4, Appli	916	423	5	PCT-US96-10986-14	Sequence 14, Appli
844	5	4.1	403	5	US-09-222-851-4	Sequence 2, Appli	917	424	1	US-08-453-472-8	Sequence 8, Appli
845	5	4.1	403	5	PCT-US95-05064-2	Sequence 2, Appli	918	424	1	US-08-038-948-2	Sequence 2, Appli
846	5	4.1	404	2	US-08-282-197C-62	Sequence 2, Appli	919	424	1	US-08-038-948-5	Sequence 5, Appli
847	5	4.1	405	4	US-09-026-408-13	Sequence 4, Appli	920	424	1	US-08-453-952-8	Sequence 8, Appli
848	5	4.1	406	1	US-08-434-881-2	Sequence 13, Appli	921	424	2	US-08-484-993B-18	Sequence 18, Appli
849	5	4.1	406	3	US-08-977-771-2	Sequence 2, Appli	922	424	2	US-08-862-903-8	Sequence 8, Appli
850	5	4.1	406	4	US-09-361-773-2	Sequence 2, Appli	923	424	2	US-08-484-158B-18	Sequence 18, Appli
851	5	4.1	408	1	US-07-841-646-7	Sequence 7, Appli	924	424	2	US-08-484-596A-18	Sequence 18, Appli
852	5	4.1	408	1	US-07-718-274A-6	Sequence 6, Appli	925	424	2	US-08-480-150A-18	Sequence 18, Appli
853	5	4.1	408	1	US-07-901-703-19	Sequence 19, Appli	926	424	3	US-08-458-731-18	Sequence 18, Appli
854	5	4.1	408	1	US-08-149-106-6	Sequence 6, Appli	927	424	3	US-08-149-223A-18	Sequence 18, Appli
855	5	4.1	408	1	US-08-147-023-7	Sequence 7, Appli	928	426	1	US-08-455-550-21	Sequence 21, Appli
856	5	4.1	408	1	US-08-298-021-6	Sequence 6, Appli	929	426	2	US-08-852-743-2	Sequence 2, Appli
857	5	4.1	408	1	US-07-951-715A-21	Sequence 21, Appli	930	426	2	US-09-211-930-4	Sequence 4, Appli
858	5	4.1	408	1	US-08-050-132A-4	Sequence 4, Appli	931	426	3	US-09-340-993-4	Sequence 4, Appli
859	5	4.1	408	1	US-08-447-570-7	Sequence 7, Appli	932	426	3	US-09-185-370-2	Sequence 2, Appli
860	5	4.1	408	2	US-08-459-346-11	Sequence 11, Appli	933	426	3	US-09-152-406-4	Sequence 4, Appli
861	5	4.1	408	2	US-08-459-448A-21	Sequence 21, Appli	934	426	4	US-09-468-442-4	Sequence 4, Appli
862	5	4.1	408	2	US-08-449-700-7	Sequence 7, Appli	935	427	4	US-09-025-580-34	Sequence 34, Appli
863	5	4.1	408	2	US-08-449-699A-7	Sequence 7, Appli	936	427	4	US-09-025-580-36	Sequence 36, Appli
864	5	4.1	408	3	US-08-459-595A-21	Sequence 21, Appli	937	429	1	US-08-218-943-3	Sequence 3, Appli
865	5	4.1	408	3	US-08-750-222A-4	Sequence 4, Appli	938	430	2	US-08-712-709-9	Sequence 9, Appli
866	5	4.1	408	3	US-08-815-652B-4	Sequence 4, Appli	939	430	3	US-09-111-444-9	Sequence 9, Appli
867	5	4.1	408	3	US-08-889-419-11	Sequence 11, Appli	940	430	3	US-09-541-228-9	Sequence 9, Appli
868	5	4.1	408	3	US-08-459-504B-21	Sequence 21, Appli	941	431	4	US-08-712-709-5	Sequence 5, Appli
869	5	4.1	408	3	US-08-459-444-21	Sequence 21, Appli	942	431	3	US-09-111-444-5	Sequence 5, Appli
870	5	4.1	408	3	US-08-459-444-21	Sequence 21, Appli	943	431	3	US-09-541-228-5	Sequence 5, Appli
871	5	4.1	408	4	US-07-721-847A-6	Sequence 6, Appli	944	434	1	US-09-741-940-5	Sequence 5, Appli
872	5	4.1	408	4	US-08-469-411-4	Sequence 4, Appli	945	434	1	US-08-289-548A-5	Sequence 5, Appli
873	5	4.1	408	4	US-08-925-779-6	Sequence 6, Appli	946	434	1	US-08-452-654-5	Sequence 5, Appli
874	5	4.1	408	4	US-08-254-353A-4	Sequence 4, Appli	947	434	1	US-08-452-655B-5	Sequence 5, Appli
875	5	4.1	408	5	PCT-US91-03540A-9	Sequence 9, Appli	948	434	3	US-08-450-582-5	Sequence 5, Appli
876	5	4.1	408	5	PCT-US92-05374A-4	Sequence 4, Appli	949	441	4	US-08-244-603A-1	Sequence 1, Appli
877	5	4.1	408	5	PCT-US93-05446-19	Sequence 19, Appli	950	442	4	US-09-081-689-2	Sequence 2, Appli
878	5	4.1	408	5	PCT-US93-07189-11	Sequence 11, Appli	951	442	6	5310667-6	Patent No. 5310667
879	5	4.1	408	6	PCT-US95-07084-4	Sequence 4, Appli	952	443	6	5310667-6	Patent No. 5310667
880	5	4.1	408	6	5166058-6	Patent No. 5166058	953	443	6	5310667-2	Patent No. 5310667
881	5	4.1	409	6	5168050-4	Patent No. 5168050	954	444	1	US-08-476-008-51	Sequence 51, Appli
882	5	4.1	410	1	US-08-792-283A-7	Sequence 7, Appli	955	444	1	US-08-476-008-52	Sequence 52, Appli
883	5	4.1	410	2	US-09-103-908-7	Sequence 7, Appli	956	444	1	US-08-476-008-53	Sequence 53, Appli
884	5	4.1	410	2	US-08-741-327E-15	Sequence 15, Appli	957	444	1	US-08-476-008-54	Sequence 54, Appli
885	5	4.1	410	4	US-09-271-713-7	Sequence 7, Appli	958	444	1	US-08-476-008-55	Sequence 55, Appli
886	5	4.1	410	4	US-09-065-872-1	Sequence 1, Appli	959	444	1	US-08-476-008-56	Sequence 56, Appli
887	5	4.1	410	4	US-09-023-809B-1	Sequence 1, Appli	960	444	1	US-08-306-063-51	Sequence 51, Appli
888	5	4.1	415	3	US-09-176-657-8	Sequence 8, Appli	961	444	1	US-08-306-063-52	Sequence 52, Appli
889	5	4.1	415	3	US-08-938-830-1	Sequence 1, Appli	962	444	1	US-08-306-063-53	Sequence 53, Appli
890	5	4.1	415	3	US-09-020-222-1	Sequence 1, Appli	963	444	1	US-08-306-063-54	Sequence 54, Appli
891	5	4.1	415	3	US-08-852-936C-1	Sequence 1, Appli	964	444	1	US-08-306-063-55	Sequence 55, Appli
892	5	4.1	416	3	US-09-257-218-2	Sequence 2, Appli	965	444	1	US-08-306-063-56	Sequence 56, Appli
893	5	4.1	416	4	US-09-311-760-2	Sequence 2, Appli	966	444	1	US-08-833-485-51	Sequence 51, Appli
894	5	4.1	416	4	US-09-300-328-1	Sequence 1, Appli	967	444	1	US-08-833-485-52	Sequence 52, Appli
895	5	4.1	419	1	US-07-841-646-19	Sequence 19, Appli	968	444	1	US-08-833-485-53	Sequence 53, Appli
896	5	4.1	419	1	US-08-147-023-19	Sequence 19, Appli	969	444	1	US-08-833-485-54	Sequence 54, Appli
897	5	4.1	419	1	US-08-295-411-1	Sequence 1, Appli	970	444	1	US-08-833-485-55	Sequence 55, Appli
898	5	4.1	419	1	US-08-447-570-19	Sequence 19, Appli	971	444	1	US-08-833-485-56	Sequence 56, Appli
899	5	4.1	419	1	US-08-553-703A-3	Sequence 3, Appli	972	444	4	US-09-243-374-2	Sequence 2, Appli
900	5	4.1	419	2	US-08-449-700-19	Sequence 19, Appli	973	444	4	US-09-243-374-3	Sequence 3, Appli
901	5	4.1	419	2	US-08-449-699A-19	Sequence 19, Appli	974	444	4	US-09-243-374-5	Sequence 5, Appli
902	5	4.1	419	2	US-08-955-471-1	Sequence 1, Appli	975	444	4	US-09-137-440-51	Sequence 51, Appli
903	5	4.1	419	2	US-09-006-021-3	Sequence 3, Appli	976	444	4		

977 5 4.1 444 4 US-09-137-440-52 Sequence 52, Appl
978 5 4.1 444 4 US-09-137-440-53 Sequence 53, Appl
979 5 4.1 444 4 US-09-137-440-54 Sequence 54, Appl
980 5 4.1 444 4 US-09-137-440-55 Sequence 55, Appl
981 5 4.1 444 4 US-09-137-440-56 Sequence 56, Appl
982 5 4.1 444 6 5310667-1 Patent No. 5310667
983 5 4.1 444 6 5310667-3 Patent No. 5310667
984 5 4.1 444 6 5310667-5 Patent No. 5310667
985 5 4.1 445 3 US-08-985-090-2 Sequence 2, Appl
986 5 4.1 445 3 US-09-165-543-2 Sequence 2, Appl
987 5 4.1 445 4 US-09-167-354-7 Sequence 7, Appl
988 5 4.1 446 3 US-08-956-254-2 Sequence 2, Appl
989 5 4.1 446 3 US-09-008-388-1 Sequence 1, Appl
990 5 4.1 446 4 US-09-243-374-4 Sequence 4, Appl
991 5 4.1 446 6 5310667-4 Patent No. 5310667
992 5 4.1 447 1 US-08-365-689-1 Sequence 1, Appl
993 5 4.1 447 1 US-07-747-781-1 Sequence 1, Appl
994 5 4.1 447 1 US-08-145-138A-1 Sequence 1, Appl
995 5 4.1 447 1 US-08-468-853-2 Sequence 2, Appl
996 5 4.1 447 1 US-08-468-855-2 Sequence 2, Appl
997 5 4.1 447 1 US-08-310-357-2 Sequence 2, Appl
998 5 4.1 447 1 US-08-468-852-2 Sequence 2, Appl
999 5 4.1 447 2 US-08-468-857-2 Sequence 2, Appl
1000 5 4.1 447 4 US-09-305-001-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-879-995A-1
; Sequence 1, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

; LIBRARY: BRAITUT03
; CLONE: 2109906
; US-08-879-995A-1

Query Match 54.5%; Score 66; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.le-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSGAVCKEPOEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPOEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Qy 61 LKALSQ 66
Db 61 LKALSQ 66

RESULT 2
US-09-215-096-1
; Sequence 1, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
; US-09-215-096-1

Query Match 54.5%; Score 66; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.le-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRIMLLFTAILAFSLAQSGAVCKEPOEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPOEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60

Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEVVGGRSKRDPDLYQLQRLFKSHSSLEGL 60
QY 61 LKALSQ 66
|||||
Db 61 LKALSQ 66

RESULT 3
US-08-879-995A-4
; Sequence 4, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 205725
; US-08-879-995A-4

Query Match 8.3%; Score 10; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVVG 88
|||||
Db 80 KRDMHDFVVG 89

RESULT 4
US-09-215-096-4
; Sequence 4, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.

; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 205725
; US-09-215-096-4

Query Match 8.3%; Score 10; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVVG 88
|||||
Db 80 KRDMHDFVVG 89

RESULT 5
US-08-879-995A-3
; Sequence 3, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 163590
US-08-879-995A-3

Query Match 8.3%; Score 10; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
|||||
DB 84 KRDHDFVVG 93

RESULT 6
US-09-215-096-3
Sequence 3, Application US/09215096
Patent No. 6008194
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 163590
US-09-215-096-3

Query Match 8.3%; Score 10; DB 3; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
|||||
DB 84 KRDHDFVVG 93

RESULT 7
US-07-899-205-3
Sequence 3, Application US/07899205
Patent No. 5288730
GENERAL INFORMATION:
APPLICANT: Baker, Raymond
APPLICANT: Teall, Martin R.
APPLICANT: Swain, Christopher J.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: AZABICYCLIC COMPOUNDS PHARMACEUTICAL
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,205
FILING DATE: 19920616
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Polk, Manfred
REGISTRATION NUMBER: 27,102
REFERENCE/DOCKET NUMBER: T-1106
TELEPHONE: (908) 594-4285
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-899-205-3

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 DMHDFVVG 88
|||||
DB 1 DMHDFVVG 8

RESULT 8
US-08-184-935-10
; Sequence 10, Application US/08184935
; Patent No. 5476770
; GENERAL INFORMATION:
; APPLICANT: PRADELLES, PHILIPPE
; TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN
; TITLE OF INVENTION: OR HAPTEN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,935
; FILING DATE: 24-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5476770man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 846-286-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /note= "C-terminal amide"
US-08-184-935-10

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8

RESULT 9
US-08-269-288-4
; Sequence 4, Application US/08269288
; Patent No. 5491140
; GENERAL INFORMATION:
; APPLICANT: Bruns, Robert F.
; APPLICANT: Gehlert, Donald R.
; APPLICANT: Howbert, James J.
; APPLICANT: Lunn, William H.W.
; TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana

COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,288
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9715
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-269-288-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8

RESULT 10
US-08-338-484-3
; Sequence 3, Application US/08338484
; Patent No. 5494926
; GENERAL INFORMATION:
; APPLICANT: Owens, Andrew P.
; APPLICANT: Teall, Martin R.
; APPLICANT: Williams, Brian J.
; TITLE OF INVENTION: 2/3-(HETEROCYCLIC ALKYL
; TITLE OF INVENTION: AMINO)-1-(SUBSTITUTED PHENYL-METHOXY)-ETHANES/PROPANES AS
; TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Robert J. No. 5494926th
; STREET: 126 E. Lincoln Ave., P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,484
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5494926th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-484-3

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098; 0; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 81 DMHDFVVG 88
|||||
Db 1 DMHDFVVG 8

RESULT 11
US-08-175-432-3
Sequence 3, Application US/08175432
Patent No. 5495047
GENERAL INFORMATION:
APPLICANT: Saari, Walfred S.
APPLICANT: Van Niel, Monique B.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: FUSED TRICYCLIC COMPOUNDS,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE
TITLE OF INVENTION: IN THERAPY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NORTH, ROBERT J.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,432
FILING DATE: 07-JAN-1994
CLASSIFICATION: 560
ATTORNEY/AGENT INFORMATION:
NAME: No. 5495047th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1152Y
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-175-432-3

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098; 0; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 81 DMHDFVVG 88
|||||
Db 1 DMHDFVVG 8

RESULT 12
US-08-462-413-4
Sequence 4, Application US/08462413
Patent No. 5530009
GENERAL INFORMATION:
APPLICANT: Cho, Sung Y.
APPLICANT: Copp, James D.
APPLICANT: Ginah, Francis O.
APPLICANT: Hansen, Guy J.
APPLICANT: Hipskind, Phillip A.
APPLICANT: Huff, Bret E.
APPLICANT: Martinelli, Michael J.
APPLICANT: Staszak, Michael A.
APPLICANT: Sharp-Taylor, Roger W.
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PEPTIDYL
TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,413
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/271,708
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9475
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-413-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098; 0; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 81 DMHDFVVG 88
|||||
Db 1 DMHDFVVG 8

RESULT 13
US-08-391-910-4
Sequence 4, Application US/08391910
Patent No. 5563133
GENERAL INFORMATION:
APPLICANT: Hipskind, Phillip A.
TITLE OF INVENTION: HEXAMETHYLENEIMINYL TACHYKININ RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9979
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-910-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8

RESULT 14
US-08-418-994-4
Sequence 4, Application US/08418994
Patent No. 555568
GENERAL INFORMATION:
APPLICANT: Cho, Sung-Yong S.
APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, J. J.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: 2-ACYLAMINOPROPANAMIDES AS TACHYKININ
RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-8252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-418-994-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8

RESULT 15
US-08-391-814-4
Sequence 4, Application US/08391814
Patent No. 5607947
GENERAL INFORMATION:
APPLICANT: Hipskind, Philip A.
TITLE OF INVENTION: PYRROLIDINYL TACHYKININ RECEPTOR
ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-814-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8

Wed May 8 10:57:56 2002

us-09-852-659-85.oligo.ra1

Page 14

Search completed: May 3, 2002, 12:28:47
Job time: 124 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:27:04 ; Search time 14.49 Seconds
(without alignments)
636.102 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRIMLLFTRAILAFSLAQSFSG.....DVNQENVPFSGILKYPRAE 121

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_68:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	8.3	116	2 A43779	neurokinin B precu
2	10	8.3	116	2 I65342	tachykinin B precu
3	10	8.3	126	2 A25905	tachykinin B precu
4	8	6.6	10	1 SPGKX	neuromedin K - pig
5	8	6.6	812	2 E75338	DNA gyrase, subuni
6	7	5.8	143	2 S75133	hypothetical prote
7	7	5.8	310	2 H70733	hypothetical prote
8	7	5.8	366	2 T50468	probable maturase
9	7	5.8	377	2 B82846	succinyl-diaminopi
10	7	5.8	394	2 E75439	conserved hypotet
11	7	5.8	475	2 C81351	probable UDP-N-ace
12	7	5.8	493	2 E96664	hypothetical prote
13	7	5.8	496	2 C83122	probable aldehyde
14	7	5.8	534	2 D83775	hypothetical prote
15	7	5.8	590	1 A54372	G protein-coupled
16	7	5.8	590	2 A48277	G protein-coupled
17	7	5.8	648	1 A64167	cytochrome c-type
18	7	5.8	702	2 A86383	hypothetical prote
19	7	5.8	712	2 T33231	hypothetical prote
20	7	5.8	1038	2 T51518	ubiquitin-fusion d
21	7	5.8	1058	2 T50496	hypothetical prote
22	7	5.8	1516	2 F84919	glutathione-conjug
23	6	5.0	20	2 FC2084	serine proteinase
24	6	5.0	35	2 P50439	potassium channel
25	6	5.0	72	1 C24033	small acid-soluble
26	6	5.0	73	1 B24543	small acid-soluble
27	6	5.0	77	2 E71367	hypothetical prote
28	6	5.0	80	2 S78706	protein YER058c-a
29	6	5.0	84	2 S48815	hypothetical prote

30	5.0	87	2	T18152	hypothetical prote
31	5.0	97	2	T25342	hypothetical prote
32	5.0	98	2	D70069	hypothetical prote
33	5.0	104	2	S56789	hypothetical prote
34	5.0	105	2	G71102	hypothetical prote
35	5.0	105	2	B82149	conserved hypotet
36	5.0	108	1	WMVP5	nucleic acid-bindi
37	5.0	108	2	S12976	12k protein - pota
38	5.0	109	2	T34135	hypothetical prote
39	5.0	110	2	S12028	hypothetical prote
40	5.0	110	2	H64512	hypothetical prote
41	5.0	118	2	S72690	probable membrane
42	5.0	130	2	C55546	flagellar protein
43	5.0	130	2	F64950	flagellar protein
44	5.0	130	2	H85800	flagellar protein
45	5.0	132	2	S14977	glycine-rich prote
46	5.0	142	2	A49296	hemoglobin alpha-B
47	5.0	143	2	T13179	hypothetical prote
48	5.0	152	1	MYPN	myoglobin - empero
49	5.0	152	2	H72578	hypothetical prote
50	5.0	153	1	MYSLG	myoglobin - gray s
51	5.0	153	1	MYSLH	myoglobin [validat
52	5.0	153	1	MYWHP	myoglobin [validat
53	5.0	153	2	JN0344	myoglobin - Baikal
54	5.0	153	2	A72483	hypothetical prote
55	5.0	154	2	S48026	ribosomal protein
56	5.0	155	2	S30953	gene 5 protein - M
57	5.0	156	2	I37222	dimeric cap bindin
58	5.0	156	2	S60109	nuclear cap bindin
59	5.0	160	2	A71300	conserved hypotet
60	5.0	162	2	D64471	hypothetical prote
61	5.0	168	2	T52480	cytochrome-c oxida
62	5.0	169	2	F69072	hypothetical prote
63	5.0	173	2	S52132	t-complex-type mol
64	5.0	173	2	T19290	hypothetical prote
65	5.0	177	2	F69365	conserved hypotet
66	5.0	179	2	S54186	outer surface prot
67	5.0	179	2	S54187	outer surface prot
68	5.0	179	2	S54188	outer surface prot
69	5.0	180	2	S54191	outer surface prot
70	5.0	182	2	E71528	probable transcrip
71	5.0	183	1	QOBPL	git protein - phag
72	5.0	191	2	H72767	hypothetical prote
73	5.0	191	2	E84740	hypothetical prote
74	5.0	191	2	F84522	probable proline-r
75	5.0	193	2	S70265	outer surface prot
76	5.0	193	2	C84405	hypothetical prote
77	5.0	193	2	T30325	hypothetical prote
78	5.0	195	2	T48864	rac-like protein A
79	5.0	196	2	T48865	GTP-binding protei
80	5.0	197	2	A47525	GTP-binding protei
81	5.0	197	2	T04705	rac-like GTP bindi
82	5.0	197	2	T08857	probable GTP-bindi
83	5.0	197	2	T45761	rac-like GTP bindi
84	5.0	198	2	T51962	Rac-like GTP bindi
85	5.0	199	2	T01596	GTP-binding protei
86	5.0	199	2	A82721	conserved hypotet
87	5.0	205	2	T46434	hypothetical prote
88	5.0	208	2	C82927	hypothetical prote
89	5.0	209	2	E64791	enterobactin synth
90	5.0	209	2	A85557	enterobactin synth
91	5.0	211	2	I40278	outer surface prot
92	5.0	212	2	S13293	KDEL receptor - hu
93	5.0	212	2	A44394	KDEL receptor - bo
94	5.0	212	2	S69921	outer surface prot
95	5.0	212	2	S20543	outer surface prot
96	5.0	219	2	T01104	disease resistance
97	5.0	219	2	H96608	hypothetical prote
98	5.0	221	2	D83471	hypothetical prote
99	5.0	223	2	E69181	conserved hypotet
100	5.0	227	2	D84381	hypothetical prote
101	5.0	228	2	C83663	hypothetical prote
102	5.0	231	2	S75387	hypothetical prote

103	231	2	S15139	23S rRNA intron 1	176	6	5.0	354	2	T24094	hypothetical prote
104	232	2	A83208	hypothetical prote	177	6	5.0	355	2	T52177	root hairless prot
105	238	2	F72522	hypothetical prote	178	6	5.0	357	2	B81396	probable aminotran
106	239	2	S52823	hypothetical prote	179	6	5.0	359	2	E83251	probable aminotran
107	239	2	T01463	hypothetical prote	180	6	5.0	359	2	S44425	angiotensin II rec
108	240	1	W2BE39	gene 39 protein -	181	6	5.0	359	2	JH0621	angiotensin II rec
109	240	2	T24957	hypothetical prote	182	6	5.0	359	2	JC2134	angiotensin II rec
110	240	2	B82833	conserved hypotet	183	6	5.0	359	2	A75438	recF protein - Del
111	241	2	T38217	probable transcrip	184	6	5.0	360	2	C64628	lipid A disacchari
112	245	1	A47539	homeotic protein g	185	6	5.0	360	2	D71888	lipid-a-disacchari
113	245	2	S78698	probable export pr	186	6	5.0	361	2	S68268	apurinic/pyrimidi
114	245	2	G86869	probable export pr	187	6	5.0	364	2	A71443	probable inositol
115	245	2	B85812	flagellar biosynth	188	6	5.0	365	2	S56792	hypothetical prote
116	246	2	T12585	Dc3 promoter-bind	189	6	5.0	366	1	S70674	hypothetical prote
117	247	2	T15579	hypothetical prote	190	6	5.0	366	2	T25178	hypothetical prote
118	248	2	B83764	transcription regu	191	6	5.0	367	2	S3172	cytochrome P450 2B
119	250	2	H82079	protein disulfide-	192	6	5.0	370	2	C83120	probable RND efflu
120	251	2	S75312	hypothetical prote	193	6	5.0	372	2	S69064	hypothetical prote
121	251	2	T24485	hypothetical prote	194	6	5.0	372	2	A41792	homeotic protein e
122	253	2	A5183	GS2 protein - huma	195	6	5.0	373	2	B96798	extensin [imported
123	258	2	S35276	probable export pr	196	6	5.0	375	2	B11842	carbamoyl-phosphat
124	261	2	H70933	hypothetical prote	197	6	5.0	375	2	E84674	carbamoyl-phosphat
125	261	2	F81376	probable integral	198	6	5.0	375	2	D75568	N-acetylamino acid r
126	267	2	T08283	hypothetical prote	199	6	5.0	377	2	B30341	G protein-coupled
127	268	1	JQ0961	myb-related protei	200	6	5.0	379	2	T11414	ubiquinol--cytochr
128	268	2	T46902	hypothetical prote	201	6	5.0	380	2	S39600	class I histocoma
129	271	2	G64025	hypothetical prote	202	6	5.0	385	1	S76874	probable hydro-ly
130	273	2	D71180	probable ribosomal	203	6	5.0	387	2	I50703	transcription fact
131	278	2	S18545	rab28 protein - ma	204	6	5.0	388	1	DEHPT	pyruvate dehydroge
132	278	2	T23291	hypothetical prote	205	6	5.0	388	2	B70878	probable transfe
133	279	2	H83811	hypothetical prote	206	6	5.0	388	2	F69536	conserved hypotet
134	281	2	A38090	N-hydroxyarylamine	207	6	5.0	390	2	G82844	cysteine synthase
135	282	2	S39972	leucine-rich prote	208	6	5.0	391	2	H70041	probable transcrip
136	283	2	A69517	conserved hypotet	209	6	5.0	392	2	S72936	UDP-glucuronosyltr
137	284	2	S71227	extensin 1 - Arabi	210	6	5.0	392	2	C72783	hypothetical prote
138	286	2	F82881	hypothetical prote	211	6	5.0	393	2	S25331	probable methionyl
139	289	2	T16530	hypothetical prote	212	6	5.0	395	2	S38812	cyclin A - chicken
140	292	2	F72208	conserved hypotet	213	6	5.0	399	1	S38656	teta protein - Pse
141	293	2	F72409	conserved hypotet	214	6	5.0	399	1	YTECRL	tetracycline resis
142	293	2	T23806	hypothetical prote	215	6	5.0	399	2	J01479	tetracycline resis
143	294	2	A57478	serine O-acetyltra	216	6	5.0	399	2	S36719	FUN33 protein - ya
144	295	2	T20629	hypothetical prote	217	6	5.0	402	1	S25077	monensin polyketid
145	300	2	S54717	probable transcrip	218	6	5.0	406	2	T21271	hypothetical prote
146	300	2	T49748	hypothetical prote	219	6	5.0	409	2	T31662	hypothetical prote
147	302	2	F75619	probable hemin ABC	220	6	5.0	411	2	B82682	succinylornithine
148	304	2	I50721	synemin - chicken	221	6	5.0	411	2	T46681	probable glycosylt
149	309	2	T43752	site-specific DNA	222	6	5.0	414	2	A72765	hypothetical prote
150	312	2	S71207	serine O-acetyltra	223	6	5.0	415	2	T44601	probable glycosylt
151	316	2	H86665	ferrichrome ABC tr	224	6	5.0	415	2	E83544	hypothetical prote
152	320	2	F89747	two-component sens	225	6	5.0	416	2	T31486	hypothetical prote
153	322	2	T40718	probable transmemb	226	6	5.0	418	2	A37344	acrosin (EC 3.4.21
154	327	1	HLHUCD	T-cell surface gly	227	6	5.0	420	2	T19800	hypothetical prote
155	328	2	S32369	gamma-SNAP protein	228	6	5.0	421	2	A55283	acrosin (EC 3.4.21
156	329	2	T23924	hypothetical prote	229	6	5.0	421	2	T49734	hypothetical prote
157	332	2	T46239	hypothetical prote	230	6	5.0	422	2	T47065	probable ATP-depen
158	333	1	HLHUCB	T-cell surface gly	231	6	5.0	430	2	C70176	citrate utilizatio
159	333	2	S76782	D-2-hydroxy-acid d	232	6	5.0	431	1	ZTEC3	citrate utilizatio
160	333	2	B96657	probable replicati	233	6	5.0	431	1	ZTEC6	probable membrane
161	334	2	G86723	exodeoxyribonuclea	234	6	5.0	431	2	T36570	hypothetical prote
162	335	1	A25968	DNA-directed RNA p	235	6	5.0	432	2	T05236	citrate carrier pr
163	335	1	HLHUR3	T-cell surface gly	236	6	5.0	434	2	JQ0576	chaperonin 60 beta
164	336	2	I56235	rat CDI antigen pr	237	6	5.0	435	2	S56644	glucose-inhibited
165	337	2	I48682	NEX-1 - mouse	238	6	5.0	435	2	A72339	probable transposa
166	337	2	S70738	gene Dlx-3 protein	239	6	5.0	439	2	H70582	hypothetical prote
167	342	2	S63654	hypothetical COI i	240	6	5.0	442	2	H72209	hypothetical prote
168	343	2	G86709	hypothetical prote	241	6	5.0	443	1	Q0BYET	aminopeptidase p x
169	344	2	JH0511	myo-inositol 2-deh	242	6	5.0	446	2	F82609	hypothetical prote
170	344	2	H83928	hypothetical prote	243	6	5.0	454	2	T42680	hypothetical prote
171	345	2	E50512	hypothetical prote	244	6	5.0	457	2	A69359	amidophosphoribosy
172	345	2	B85881	hypothetical prote	245	6	5.0	457	2	E96572	protein F12W16.8 [
173	347	2	T09140	serine O-acetyltra	246	6	5.0	464	2	A28569	alpha-methyl dopa-h
174	347	2	S76278	ABC-type transport	247	6	5.0	470	2	D83938	hypothetical prote
175	349	1	G64096	D-galactose-bindin	248	6	5.0	472	2	T22188	hypothetical prote

249	6	5.0	477	2	H86466	protein F23M19.7 [322	6	5.0	621	2	A83421	peptidyl-prolyl ci
250	6	5.0	479	1	A54040	adenosylhomocystei	323	6	5.0	633	2	T47524	hypothetical prote
251	6	5.0	481	2	S47091	cyclase-associated	324	6	5.0	635	2	C81861	hypothetical prote
252	6	5.0	481	2	T39357	hypothetical prote	325	6	5.0	640	2	T08758	hypothetical prote
253	6	5.0	484	2	S67820	GumD protein - xan	326	6	5.0	654	2	B84690	hypothetical prote
254	6	5.0	485	2	T04840	hypothetical prote	327	6	5.0	658	1	S73805	DNA ligase (NAD+)
255	6	5.0	491	1	O4RTPB	cytochrome P450 2B	328	6	5.0	663	2	T30621	hypothetical prote
256	6	5.0	491	1	O4RTPE	cytochrome P450 2B	329	6	5.0	667	2	S66017	formate dehydrogen
257	6	5.0	491	1	O4RBPC	cytochrome P450 2B	330	6	5.0	670	1	E70040	conserved dehydrog
258	6	5.0	491	2	JT0676	cytochrome P450 2B	331	6	5.0	671	2	D84648	probable disease r
259	6	5.0	491	2	S31277	cytochrome P450 2B	332	6	5.0	671	2	E82960	hypothetical prote
260	6	5.0	491	2	S31278	cytochrome P450 2B	333	6	5.0	684	2	T43452	hypothetical prote
261	6	5.0	491	2	S35666	cytochrome P450 2B	334	6	5.0	686	2	T06700	hypothetical prote
262	6	5.0	491	2	A27717	cytochrome P450 2B	335	6	5.0	690	2	E84724	hypothetical prote
263	6	5.0	491	2	A31047	testosterone 16alp	336	6	5.0	695	2	T07283	hypothetical prote
264	6	5.0	491	2	A32969	cytochrome P450 2B	337	6	5.0	698	2	D84547	hypothetical prote
265	6	5.0	491	2	T49625	testosterone 16a-h	338	6	5.0	701	2	D83677	hypothetical prote
266	6	5.0	491	2	T84735	testosterone 16a-h	339	6	5.0	704	2	S46000	probable membrane
267	6	5.0	492	2	S27160	cytochrome P450 2B	340	6	5.0	725	1	Z2BEA4	rapid lysis protei
268	6	5.0	494	2	S11305	cytochrome P450 2B	341	6	5.0	727	2	T26096	hypothetical prote
269	6	5.0	497	2	T32728	hypothetical prote	342	6	5.0	727	2	A54051	glycerol-3-phospha
270	6	5.0	499	2	B81914	probable periplasm	343	6	5.0	728	1	S59553	arginine decarboxy
271	6	5.0	500	2	B31047	testosterone 16alp	344	6	5.0	731	2	T44846	catalase (EC 1.11.
272	6	5.0	502	2	A82234	gonadoliberin III-	345	6	5.0	737	2	S47857	basic protein, cyt
273	6	5.0	507	2	T26809	hypothetical prote	346	6	5.0	738	2	A53542	brefeldin A-sensit
274	6	5.0	507	2	S23348	hypothetical prote	347	6	5.0	739	2	T15215	hypothetical prote
275	6	5.0	509	2	I45713	Dpp receptor TRV,	348	6	5.0	744	2	A70385	DNA gyrase A subun
276	6	5.0	509	2	G82809	amino acid transpo	349	6	5.0	751	2	F83080	hypothetical prote
277	6	5.0	510	2	S77380	lysine--trNA ligas	350	6	5.0	752	2	G82798	hypothetical prote
278	6	5.0	510	2	A32380	nuclear protein fk	351	6	5.0	760	2	H84427	hypothetical prote
279	6	5.0	511	2	E75561	probable phytoene	352	6	5.0	761	2	E85359	hypothetical prote
280	6	5.0	512	2	S06115	alpha-amylase (EC	353	6	5.0	779	1	S40382	box A-binding fact
281	6	5.0	512	2	S23355	alpha-amylase (EC	354	6	5.0	800	2	S13032	3',5'-cyclic-GMP p
282	6	5.0	513	2	T49365	hypothetical prote	355	6	5.0	800	2	H84740	hypothetical prote
283	6	5.0	513	2	C82366	conserved hypotet	356	6	5.0	802	1	A37142	outer membrane ush
284	6	5.0	516	2	S42093	cellulose 1,4-beta	357	6	5.0	803	2	A86655	hypothetical prote
285	6	5.0	519	2	A82634	2-isopropylmalate	358	6	5.0	804	2	D72257	DNA gyrase, subuni
286	6	5.0	526	2	T41944	hypothetical prote	359	6	5.0	809	2	G75605	hypothetical prote
287	6	5.0	527	1	T42934	thymidine kinase (360	6	5.0	810	2	S75931	hypothetical prote
288	6	5.0	527	2	S12158	hypothetical prote	361	6	5.0	810	2	D6818	hypothetical prote
289	6	5.0	529	2	B24059	t complex polypept	362	6	5.0	812	2	T07745	phosphatidylinosit
290	6	5.0	530	2	A81323	arginine--trNA lig	363	6	5.0	814	2	T07761	phosphatidylinosit
291	6	5.0	534	2	T29059	probable 2-isoprop	364	6	5.0	818	2	T01105	disease resistance
292	6	5.0	545	2	S51563	heat shock protein	365	6	5.0	820	2	H82302	Atp-dependent heli
293	6	5.0	545	2	H70180	heat shock protein	366	6	5.0	823	2	F64526	adenine/cytosine D
294	6	5.0	547	2	I40331	Cpn60 protein (Gro	367	6	5.0	824	2	F72408	leucine--trNA liga
295	6	5.0	547	2	B43606	heat shock protein	368	6	5.0	824	2	I52835	H-NUC - human
296	6	5.0	547	2	B83098	GroEL protein PA43	369	6	5.0	831	2	D96639	protein Tlf9.12 [i
297	6	5.0	549	2	C83677	L-lactate permease	370	6	5.0	831	2	S26675	DNA-directed DNA p
298	6	5.0	550	2	S61297	heat-shock protein	371	6	5.0	831	2	JX0359	DNA-directed DNA p
299	6	5.0	551	2	S30691	arylsulfatase (EC	372	6	5.0	832	2	A33530	DNA-directed DNA p
300	6	5.0	551	2	E86066	arylsulfatase [imp	373	6	5.0	835	2	T26086	hypothetical prote
301	6	5.0	552	2	S39765	chaperonin 60 - Co	374	6	5.0	849	2	H84546	hypothetical prote
302	6	5.0	553	2	S53080	hypothetical prote	375	6	5.0	853	2	A36617	3',5'-cyclic-GMP p
303	6	5.0	554	2	T36653	probable cation tr	376	6	5.0	854	2	A42828	3',5'-cyclic-GMP p
304	6	5.0	556	2	S13163	t-complex-type mol	377	6	5.0	856	2	S30762	3',5'-cyclic-GMP p
305	6	5.0	556	2	S10486	t-complex-type mol	378	6	5.0	864	2	T10970	DNA topoisomerase
306	6	5.0	556	2	JH0475	t complex polypept	379	6	5.0	864	2	D84740	hypothetical prote
307	6	5.0	556	2	JC1443	t complex polypept	380	6	5.0	887	2	S43196	uridyllyltransfera
308	6	5.0	556	2	JQ0866	t-complex protein	381	6	5.0	889	2	T09055	uridyllyltransfera
309	6	5.0	556	2	T39383	t-complex protein	382	6	5.0	890	2	G64740	uridyllyltransfera
310	6	5.0	559	2	T39793	t-complex-type mol	383	6	5.0	890	2	A85501	hypothetical prote
311	6	5.0	565	2	T23843	hypothetical prote	384	6	5.0	890	2	A30481	bacteriocin BCN5 -
312	6	5.0	568	2	B86400	hypothetical prote	385	6	5.0	890	2	T00800	disease resistance
313	6	5.0	570	2	T46911	hypothetical prote	386	6	5.0	895	2	E64431	UDPglucose 6-dehyd
314	6	5.0	572	1	S28762	gene Dbp73D protei	387	6	5.0	896	2	H86762	ABC transporter pe
315	6	5.0	576	2	A48765	g protein-coupled	388	6	5.0	907	2	E96636	hypothetical prote
316	6	5.0	594	2	T45842	calcium dependent	389	6	5.0	908	2	C70168	DNA polymerase I (
317	6	5.0	598	2	T42070	protein serine/thr	390	6	5.0	922	2	T37256	metalloproteinase
318	6	5.0	602	2	G81654	conserved hypotet	391	6	5.0	932	2	S47597	mutL protein homol
319	6	5.0	602	2	F71496	hypothetical prote	392	6	5.0	934	2	T02742	probable ligand-ga
320	6	5.0	605	2	T19818	hypothetical prote	393	6	5.0	942	2	T19553	hypothetical prote
321	6	5.0	611	2	F82442	probable peptide A	394	6	5.0	944	2	S01909	hairy wing suppres

395	6	5.0	958	2	T26258	hypothetical prote	468	5	4.1	36	2	B31872	retinoic acid-bind
396	6	5.0	977	2	I52657	seizure-related pr	469	5	4.1	36	2	JA0173	basic peptide - w
397	6	5.0	984	2	T44496	cellulose 1,4-beta	470	5	4.1	39	2	C22102	phycoerythrin-545
398	6	5.0	989	2	T15576	hypothetical prote	471	5	4.1	40	2	C53288	major pollen aller
399	6	5.0	1004	2	S51133	hypothetical prote	472	5	4.1	40	2	C53288	nephritogenic prot
400	6	5.0	1007	2	T33285	transposase Tn4652	473	5	4.1	42	4	A39124	frame shifted G12_
401	6	5.0	1008	2	T05578	hypothetical prote	474	5	4.1	42	4	A39071	metallothionein -
402	6	5.0	1014	2	S75724	hypothetical prote	475	5	4.1	43	2	S18173	metallothionein -
403	6	5.0	1018	2	T15297	hypothetical prote	476	5	4.1	43	2	S18174	metallothionein -
404	6	5.0	1021	2	A28199	hypothetical prote	477	5	4.1	43	2	S33382	metallothionein -
405	6	5.0	1024	2	T21619	hypothetical prote	478	5	4.1	44	2	T07762	ribosomal protein
406	6	5.0	1047	2	T16169	hypothetical prote	479	5	4.1	45	2	S28397	T-complex protein
407	6	5.0	1055	2	T32782	hypothetical prote	480	5	4.1	45	2	A84143	hypothetical prote
408	6	5.0	1063	2	T31111	ATPase 1 (EC 3.6.1	481	5	4.1	46	2	G70224	hypothetical prote
409	6	5.0	1063	1	S06206	grainy-head protei	482	5	4.1	48	1	R5VF32	ribosomal protein
410	6	5.0	1082	2	D86731	hypothetical prote	483	5	4.1	49	2	D82447	hypothetical prote
411	6	5.0	1160	2	T31112	ATPase 2 (EC 3.6.1	484	5	4.1	50	2	S32546	cytochrome c555 -
412	6	5.0	1160	2	T23713	hypothetical prote	485	5	4.1	50	2	H85588	hypothetical prote
413	6	5.0	1197	2	T28628	Y4CA protein - Rhl	486	5	4.1	50	2	A47694	nitrate reductase
414	6	5.0	1225	2	T32555	probable C2 domain	487	5	4.1	52	2	H82682	hypothetical prote
415	6	5.0	1226	2	E82328	5-methyltetrahydro	488	5	4.1	53	2	H82612	hypothetical prote
416	6	5.0	1230	2	S56850	SMC1 protein homol	489	5	4.1	54	2	H81933	hypothetical prote
417	6	5.0	1234	2	E83415	methionine synthas	490	5	4.1	55	1	R5NT32	ribosomal protein
418	6	5.0	1250	2	E81339	probable restricti	491	5	4.1	55	2	A24633	M protein - Strept
419	6	5.0	1273	1	TDETLT	leukocyte common a	492	5	4.1	55	2	T09464	H+-transporting At
420	6	5.0	1276	1	DVMS2	multidrug resistan	493	5	4.1	56	2	A27579	T-cell receptor be
421	6	5.0	1277	1	JH051C	multidrug resistan	494	5	4.1	57	2	F81889	hypothetical prote
422	6	5.0	1278	2	S41646	p-glycoprotein - r	495	5	4.1	57	2	D81226	hypothetical prote
423	6	5.0	1281	2	I48123	p-glycoprotein iso	496	5	4.1	58	2	B25486	T-kininogen, LMW I
424	6	5.0	1286	2	T23714	hypothetical prote	497	5	4.1	58	2	T07400	TPS11 protein, pho
425	6	5.0	1295	2	T30528	reverse transcript	498	5	4.1	59	2	B69359	LSU ribosomal prot
426	6	5.0	1307	2	T23106	hypothetical prote	499	5	4.1	59	2	D69807	hypothetical prote
427	6	5.0	1371	1	VCBEM7	hypothetical prote	500	5	4.1	60	2	S62188	hypothetical prote
428	6	5.0	1371	2	T42938	major capsid prote	501	5	4.1	61	2	S75172	hypothetical prote
429	6	5.0	1413	2	G84790	probable ABC trans	502	5	4.1	61	2	A83979	hypothetical prote
430	6	5.0	1421	2	T02501	hypothetical prote	503	5	4.1	63	2	C34620	metallothionein -
431	6	5.0	1445	2	T50508	hypothetical prote	504	5	4.1	63	2	S08191	metallothionein 2
432	6	5.0	1450	2	T45888	hypothetical prote	505	5	4.1	63	2	S33381	metallothionein -
433	6	5.0	1510	2	T33100	ABC transporter-li	506	5	4.1	63	2	A34620	metallothionein -
434	6	5.0	1519	2	S41525	hypothetical prote	507	5	4.1	64	2	B69289	conserved hypotet
435	6	5.0	1533	2	T00344	major ring-forming	508	5	4.1	64	2	B69384	conserved hypotet
436	6	5.0	1547	2	T13847	hypothetical prote	509	5	4.1	64	2	B69384	hypothetical prote
437	6	5.0	1622	2	JE0378	sno (cytosine-5)-	510	5	4.1	65	2	E82738	glucan endo-1,3-be
438	6	5.0	1630	2	S64403	ESPI protein - yea	511	5	4.1	65	2	T06349	hypothetical prote
439	6	5.0	1711	2	T21432	hypothetical prote	512	5	4.1	65	2	S34538	hypothetical prote
440	6	5.0	1724	2	T13942	UNC-13-B protein -	513	5	4.1	68	1	G64421	hypothetical prote
441	6	5.0	1768	2	T13349	parallel sister ch	514	5	4.1	69	2	A05061	hypothetical prote
442	6	5.0	1784	2	C96615	hypothetical prote	515	5	4.1	69	2	F49410	t-complex polypept
443	6	5.0	1872	2	T30888	vitellogenin - Ath	516	5	4.1	69	2	T04350	auxin-induced prot
444	6	5.0	1963	1	MWKK	myosin heavy chain	517	5	4.1	69	2	PS0368	protein-tyrosine-p
445	6	5.0	2131	2	S01446	hypothetical prote	518	5	4.1	70	2	T07575	ribosomal protein
446	6	5.0	2274	2	T30258	adenomatous polypo	519	5	4.1	70	2	G42524	A-ORF-K protein -
447	6	5.0	2374	2	T21052	hypothetical prote	520	5	4.1	71	2	I49258	fibrosin - mouse (
448	6	5.0	2405	2	T08164	dynein alpha heavy	521	5	4.1	72	2	S32933	hypothetical prote
449	6	5.0	2489	2	S59782	probable membrane	522	5	4.1	72	2	C39370	hypothetical prote
450	6	5.0	2609	2	T40399	probable transport	523	5	4.1	73	2	T16615	hypothetical prote
451	6	5.0	2670	2	T37919	GCN1 homolog - fis	524	5	4.1	73	2	T31216	hypothetical prote
452	6	5.0	2769	1	UIBO	thyroglobulin prec	525	5	4.1	73	2	T31216	hypothetical prote
453	6	5.0	3161	2	T30342	protein HMWp1 - ye	526	5	4.1	74	2	A71572	hypothetical prote
454	6	5.0	3163	2	T17440	probable polyketid	527	5	4.1	74	2	I51092	gonadotropin relea
455	6	5.0	3421	1	WZBEB6	367K tegument prot	528	5	4.1	74	2	F81671	conserved hypotet
456	6	5.0	3534	2	T42567	tegument protein 2	529	5	4.1	74	2	F83837	hypothetical prote
457	6	5.0	9376	2	T14593	syringomycin synth	530	5	4.1	75	2	S63585	RNA-directed DNA p
458	6	4.1	7	2	E61491	seed protein ws-5	531	5	4.1	77	2	S45375	ribosomal protein
459	5	4.1	19	2	S19532	globin - polychaet	532	5	4.1	77	2	T04345	auxin-induced prot
460	5	4.1	21	2	S78575	protein kinase C i	533	5	4.1	77	2	S30988	gene 43 protein -
461	5	4.1	30	2	S55462	mer5 protein homol	534	5	4.1	77	2	T34983	very hypotetical
462	5	4.1	30	2	C85851	hypothetical prote	535	5	4.1	77	2	T01280	hypothetical prote
463	5	4.1	30	2	S74112	proline-rich antib	536	5	4.1	78	2	S11923	gas-vesicle protei
464	5	4.1	30	4	S12902	diphtheria toxin f	537	5	4.1	78	2	G69033	conserved hypotet
465	5	4.1	31	2	I52232	tau protein - huma	538	5	4.1	78	2	S75256	tyrosine--tRNA lig
466	5	4.1	33	2	A03150	retinoic acid-bind	539	5	4.1	78	2	S24710	ig alpha chain - h
467	5	4.1	36	2	A29164	cartilage proteogl	540	5	4.1	78	2	F83869	hypothetical prote

541 5 4.1 79 1 A58656 adipokinetic hormo
542 5 4.1 79 2 S53837 H+transporting AR
543 5 4.1 79 2 T04352 auxin-induced prot
544 5 4.1 79 2 C71901 hypothetichal prote
545 5 4.1 80 2 T17813 hypothetichal prote
546 5 4.1 80 2 T28256 ORF MSV095 hypothe
547 5 4.1 81 2 B69958 hypothetichal prote
548 5 4.1 81 2 T36197 probable acyl carr
549 5 4.1 81 2 E84002 hypothetichal prote
550 5 4.1 82 2 I50966 MHC class II beta
551 5 4.1 82 2 I50973 MHC class II beta
552 5 4.1 82 2 T32273 ribosomal protein
553 5 4.1 82 2 B28945 ranatensin precurs
554 5 4.1 82 2 D69087 hydrogenase expres
555 5 4.1 82 2 E84301 hypothetichal prote
556 5 4.1 82 2 T30135 hypothetichal prote
557 5 4.1 82 2 I51180 gonadotropin-relea
558 5 4.1 82 2 I51355 gonadotropin relea
559 5 4.1 82 2 I51365 gonadotropin-relea
560 5 4.1 82 2 I51331 gonadotropin relea
561 5 4.1 82 2 T00185 hypothetichal prote
562 5 4.1 83 2 S04884 seed protein (clon
563 5 4.1 83 2 T18122 hypothetichal prote
564 5 4.1 84 2 T07939 embryonic abundant
565 5 4.1 84 2 E83004 glutaredoxin PA512
566 5 4.1 84 2 E82510 hypothetichal prote
567 5 4.1 84 2 E64032 hypothetichal prote
568 5 4.1 84 2 G64364 hypothetichal prote
569 5 4.1 84 2 S57545 probable membrane
570 5 4.1 84 2 F72497 hypothetichal prote
571 5 4.1 85 2 T31530 hypothetichal prote
572 5 4.1 86 2 S78488 Ig kappa chain V r
573 5 4.1 86 2 G42523 A-ORF-B protein -
574 5 4.1 87 2 S69490 bombyxin B-10 - si
575 5 4.1 87 2 J00836 bombyxin B-10 - si
576 5 4.1 87 2 A82756 hypothetichal prote
577 5 4.1 88 2 T31230 hypothetichal prote
578 5 4.1 89 2 B86833 hypothetichal prote
579 5 4.1 89 2 J02361 wheat aluminum ind
580 5 4.1 90 2 J07395 salmon-type gonado
581 5 4.1 90 2 A23735 gonadoliberin prec
582 5 4.1 90 2 I51095 gonadoliberin prec
583 5 4.1 91 2 T11359 NADH dehydrogenase
584 5 4.1 91 2 S16249 embryonic abundant
585 5 4.1 91 2 T09285 embryonic abundant
586 5 4.1 91 2 T09293 hypothetichal prote
587 5 4.1 91 2 E86512 hypothetichal prote
588 5 4.1 91 2 C64539 hypothetichal prote
589 5 4.1 91 2 A71968 Mutr/hudix family
590 5 4.1 91 2 D55561 hypothetichal prote
591 5 4.1 91 2 S54546 hypothetichal prote
592 5 4.1 91 2 D72109 hypothetichal prote
593 5 4.1 92 2 I50644 gonadoliberin I pr
594 5 4.1 92 2 S32527 embryonic abundant
595 5 4.1 92 2 JQ2273 embryonic abundant
596 5 4.1 92 2 S34802 embryogenic abunda
597 5 4.1 92 2 T1372 embryonic abundant
598 5 4.1 92 2 B82066 phosphocarrier pro
599 5 4.1 92 2 S76007 hypothetichal prote
600 5 4.1 92 2 D81731 conserved hypothet
601 5 4.1 93 2 S43333 embryonic abundant
602 5 4.1 93 2 S46303 gB19.lb protein -
603 5 4.1 93 2 S43332 EmH5 protein - whe
604 5 4.1 93 2 S23749 embryonic abundant
605 5 4.1 93 2 A27519 Em protein - whea
606 5 4.1 93 2 G64641 conserved hypothet
607 5 4.1 93 2 H71872 glu-tRNA amidotran
608 5 4.1 93 2 E64336 conserved hypothet
609 5 4.1 93 2 A85839 hypothetichal prote
610 5 4.1 93 2 T72339 hypothetichal prote
611 5 4.1 94 1 VUMTEM embryonic abundant
612 5 4.1 94 2 S30186 NADH dehydrogenase
613 5 4.1 95 2 A61629 retinoic acid-bind

614 5 4.1 95 2 S22483 embryonic abundant
615 5 4.1 95 2 E86447 protein F5D14.5 [1
616 5 4.1 95 2 B71571 hypothetichal prote
617 5 4.1 96 2 S73002 hypothetichal prote
618 5 4.1 97 1 D69961 lipoprotein homolo
619 5 4.1 97 2 S16028 Ig heavy chain V r
620 5 4.1 97 2 T17861 hypothetichal prote
621 5 4.1 98 2 T14136 NADH dehydrogenase
622 5 4.1 98 2 I57601 tubulin alpha chai
623 5 4.1 98 2 G64693 hypothetichal prote
624 5 4.1 98 2 D71807 hypothetichal prote
625 5 4.1 98 2 E82394 hypothetichal prote
626 5 4.1 98 2 T36896 hypothetichal prote
627 5 4.1 99 2 T10839 embryonic abundant
628 5 4.1 99 2 G64469 hypothetichal prote
629 5 4.1 99 2 T02894 hypothetichal prote
630 5 4.1 100 1 A36138 urease (EC 3.5.1.5
631 5 4.1 100 1 B43719 urease (EC 3.5.1.5
632 5 4.1 100 1 S08478 urease (EC 3.5.1.5
633 5 4.1 100 2 B47090 urease (EC 3.5.1.5
634 5 4.1 100 2 D85603 probable urease st
635 5 4.1 100 2 E85654 probable urease st
636 5 4.1 100 2 S13796 retinoic acid-bind
637 5 4.1 100 2 D96528 protein F27115.8 [1
638 5 4.1 100 2 C84642 probable steroid b
639 5 4.1 101 2 S46383 ribosomal protein
640 5 4.1 101 2 C72741 hypothetichal prote
641 5 4.1 101 2 S69785 prgJ protein - Sal
642 5 4.1 101 2 B72638 hypothetichal prote
643 5 4.1 102 2 B49056 T-cell receptor al
644 5 4.1 102 2 S19225 embryonic abundant
645 5 4.1 102 2 H81322 probable efflux pr
646 5 4.1 102 2 T33558 hypothetichal prote
647 5 4.1 102 2 E72619 hypothetichal prote
648 5 4.1 103 2 S40134 T-cell receptor V-
649 5 4.1 103 2 G75513 conserved hypothet
650 5 4.1 103 2 C86411 protein F1K3.22 [1
651 5 4.1 104 2 T36424 probable ABC-type
652 5 4.1 105 2 T07087 embryonic abundant
653 5 4.1 105 2 S11410 hypothetichal prote
654 5 4.1 105 2 H72736 hypothetichal prote
655 5 4.1 105 2 B75035 hypothetichal prote
656 5 4.1 105 4 S59325 hypothetichal prote
657 5 4.1 106 2 F70081 hypothetichal prote
658 5 4.1 106 2 S32964 hypothetichal prote
659 5 4.1 106 2 B71659 hypothetichal prote
660 5 4.1 106 2 E82605 conjugal transfer
661 5 4.1 106 2 H64345 hypothetichal prote
662 5 4.1 106 2 B61600 segmentation prote
663 5 4.1 106 2 E84056 chloroedoxin H1 BH3
664 5 4.1 107 1 YVBPL lysis protein S -
665 5 4.1 107 2 F71604 ribosomal protein
666 5 4.1 107 2 S64117 hypothetichal prote
667 5 4.1 107 2 S18529 hypothetichal prote
668 5 4.1 107 2 D70598 hypothetichal prote
669 5 4.1 107 2 H82558 hypothetichal prote
670 5 4.1 108 1 JLB06 coupling factor 6
671 5 4.1 108 1 HMIH2 hemagglutinin prec
672 5 4.1 108 1 YVBPS2 lysis protein S -
673 5 4.1 108 2 S24251 Ig heavy chain V r
674 5 4.1 108 2 J70563 coupling factor 6
675 5 4.1 108 2 C64463 hypothetichal prote
676 5 4.1 108 2 G83073 hypothetichal prote
677 5 4.1 108 2 A28667 hypothetichal prote
678 5 4.1 108 2 G70694 hypothetichal prote
679 5 4.1 109 2 E81231 50S ribosomal prot
680 5 4.1 109 2 T01654 ribosomal protein
681 5 4.1 109 2 B72213 conserved hypothet
682 5 4.1 109 2 S73589 hypothetichal prote
683 5 4.1 109 2 B54743 transcription fact
684 5 4.1 110 1 R5BYAL acidic ribosomal p
685 5 4.1 110 2 A72728 hypothetichal prote
686 5 4.1 110 2 T33508 hypothetichal prote

687	5	4.1	111	2	S75752	hypothetical prote	104	5	4.1	124	2	D84319	30S ribosomal prot
688	5	4.1	111	2	JH0183	Sc4 protein - brac	760	5	4.1	124	2	F81942	probable regulator
689	5	4.1	111	2	T17582	hypothetical prote	761	5	4.1	124	2	A81163	conserved hypothet
690	5	4.1	111	2	A25573	minicircle a prote	762	5	4.1	124	2	A83707	hypothetical prote
691	5	4.1	111	2	T43426	glucosamine-phosph	763	5	4.1	125	2	A29879	mesotocin / neurop
692	5	4.1	112	1	SPRFA	substance P alpha	764	5	4.1	125	2	I52650	microtubule-associ
693	5	4.1	112	2	A27889	Ig heavy chain v r	765	5	4.1	125	2	D82380	chemotaxis protein
694	5	4.1	112	2	T10827	embryonic abundant	766	5	4.1	125	2	S21329	14K inner membrane
695	5	4.1	112	2	S46188	embryonic abundant	767	5	4.1	125	2	D70732	hypothetical prote
696	5	4.1	112	2	E70433	flagellar switch p	768	5	4.1	125	2	C64777	probable membrane
697	5	4.1	112	2	C54743	transcription fact	769	5	4.1	125	2	E85544	probable gene 58 p
698	5	4.1	112	2	B35308	CAMP-regulated pho	770	5	4.1	125	2	B83521	hypothetical prote
699	5	4.1	113	2	S13494	major oleosin chal	771	5	4.1	125	2	A35003	galactose-binding
700	5	4.1	113	2	S59116	programmed cell de	772	5	4.1	125	2	C83704	hypothetical prote
701	5	4.1	113	2	T17503	hypothetical prote	773	5	4.1	125	2	S29303	hypothetical prote
702	5	4.1	113	2	T09627	positive transcrip	774	5	4.1	126	2	T48831	hypothetical prote
703	5	4.1	114	2	D83373	conserved hypothet	775	5	4.1	126	2	F72729	hypothetical prote
704	5	4.1	114	2	S02049	hypothetical prote	776	5	4.1	126	2	D72570	hypothetical prote
705	5	4.1	114	2	T13529	hypothetical prote	777	5	4.1	126	2	F83536	hypothetical prote
706	5	4.1	114	2	T13324	hypothetical prote	778	5	4.1	126	2	E84225	probable ring-clea
707	5	4.1	114	2	H69894	delta-endotoxin ho	779	5	4.1	127	2	S16685	hypothetical prote
708	5	4.1	115	1	A33323	motilin precursor	780	5	4.1	128	2	S76759	Ig heavy chain v r
709	5	4.1	115	1	S37176	ribosomal protein	781	5	4.1	128	2	T08625	hypothetical prote
710	5	4.1	115	2	JC6511	motilin precursor	782	5	4.1	128	2	SPHUB	phycocerythrin alph
711	5	4.1	115	2	PH1557	Ig heavy chain v r	783	5	4.1	129	1	S69862	neurokinin 1 precu
712	5	4.1	115	2	D70123	ribosomal protein	784	5	4.1	129	2	S63422	hypothetical prote
713	5	4.1	115	2	S73268	photosystem II pro	785	5	4.1	129	2	S55044	probable membrane
714	5	4.1	115	2	F71532	hypothetical prote	786	5	4.1	129	2	C86771	NK-lysin protein -
715	5	4.1	115	2	T44558	hypothetical prote	787	5	4.1	129	2	G82095	hypothetical prote
716	5	4.1	115	2	A28336	hypothetical prote	788	5	4.1	129	2	SPRTB	transcription regu
717	5	4.1	115	2	A37258	hypothetical prote	789	5	4.1	130	1	S47038	substance P beta p
718	5	4.1	115	2	B83058	hypothetical prote	790	5	4.1	130	1	I52526	neurokinin 1 precu
719	5	4.1	116	1	B64034	ribosomal protein	791	5	4.1	130	2	S47038	tachykinin 1 precu
720	5	4.1	116	2	T04060	conserved hypothet	792	5	4.1	130	2	S37715	hypothetical prote
721	5	4.1	116	2	T14876	hypothetical prote	793	5	4.1	131	1	E93304	conserved hypothet
722	5	4.1	116	2	T33195	hypothetical prote	794	5	4.1	131	2	F82331	hypothetical prote
723	5	4.1	116	2	E72622	hypothetical prote	795	5	4.1	131	2	S09893	hypothetical prote
724	5	4.1	117	2	A28846	hypothetical prote	796	5	4.1	131	2	C83546	hypothetical prote
725	5	4.1	118	2	T43791	Ig heavy chain pre	797	5	4.1	131	2	A64649	hypothetical prote
726	5	4.1	118	2	I50813	non-specific lipid	798	5	4.1	131	2	T11570	hypothetical prote
727	5	4.1	118	2	I50814	MHC class I protei	799	5	4.1	131	2	B60725	hypothetical prote
728	5	4.1	118	2	S51207	cruxhalorhodopsin-	800	5	4.1	131	2	C72636	hypothetical prote
729	5	4.1	118	2	S45096	13K transport prot	801	5	4.1	131	2	T30643	hypothetical prote
730	5	4.1	118	2	S45099	13K transport prot	802	5	4.1	132	2	S15966	hypothetical prote
731	5	4.1	118	2	F59332	probable membrane	803	5	4.1	132	2	D82278	hypothetical prote
732	5	4.1	118	2	S64344	hypothetical prote	804	5	4.1	132	2	G84274	hypothetical prote
733	5	4.1	118	2	A32245	hypothetical prote	805	5	4.1	132	2	T08676	hypothetical prote
734	5	4.1	118	2	B81242	hypothetical prote	806	5	4.1	132	2	S36751	embryonic abundant
735	5	4.1	118	2	T27456	hypothetical prote	807	5	4.1	133	2	F70470	conserved hypothet
736	5	4.1	118	2	H72644	hypothetical prote	808	5	4.1	133	2	T26268	hypothetical prote
737	5	4.1	119	2	A65014	probable arabinoga	809	5	4.1	133	2	T39730	40S ribosomal prot
738	5	4.1	119	2	E85882	yfec protein - Esc	810	5	4.1	134	2	B69353	conserved hypothet
739	5	4.1	119	2	D75111	hypothetical prote	811	5	4.1	134	2	S75224	hypothetical prote
740	5	4.1	119	2	E72714	hypothetical prote	812	5	4.1	134	2	C75352	conserved hypothet
741	5	4.1	120	1	ZBBPG4	probable ribosomal	813	5	4.1	134	2	D82589	hypothetical prote
742	5	4.1	120	2	S27251	gene B protein - p	814	5	4.1	135	2	F84678	hypothetical prote
743	5	4.1	120	2	B72770	NADH dehydrogenase	815	5	4.1	135	2	D81337	probable ATP /GTP-
744	5	4.1	120	2	T16015	hypothetical prote	816	5	4.1	135	2	S72964	hypothetical prote
745	5	4.1	120	2	E81095	hypothetical prote	817	5	4.1	135	2	A32317	sex-regulated prot
746	5	4.1	120	2	A84286	hypothetical prote	818	5	4.1	136	2	PH1559	Ig heavy chain v r
747	5	4.1	121	2	H27888	membrane anchor li	819	5	4.1	136	2	D70361	transcription regu
748	5	4.1	121	2	D27888	Ig heavy chain v r	820	5	4.1	136	2	T03208	hypothetical prote
749	5	4.1	121	2	F84868	hypothetical prote	821	5	4.1	136	2	T36547	hypothetical prote
750	5	4.1	121	2	F70208	conserved hypothet	822	5	4.1	136	2	T46432	hypothetical prote
751	5	4.1	121	2	B96647	hypothetical prote	823	5	4.1	136	2	RJH01	retinoic acid-bind
752	5	4.1	122	2	S56024	hypothetical prote	824	5	4.1	137	1	RJBOA	retinoic acid-bind
753	5	4.1	122	2	C82926	hypothetical prote	825	5	4.1	137	2	PH1562	Ig heavy chain v r
754	5	4.1	123	2	G27888	hypothetical prote	826	5	4.1	137	2	A35825	retinoic acid-bind
755	5	4.1	123	2	A39266	Ig heavy chain v r	827	5	4.1	137	2	T04930	glycine-rich cell
756	5	4.1	123	2	S64246	heat shock protein	828	5	4.1	137	2	B55220	hypothetical prote
757	5	4.1	123	2	G84592	hypothetical prote	829	5	4.1	137	2	T02013	mitogen-activated
758	5	4.1	123	2	D72579	hypothetical prote	830	5	4.1	137	2		
759	5	4.1	124	2	I27888	Ig heavy chain v r	831	5	4.1	137	2		
						832	5	4.1	137	2			

833	5	4.1	138	1	SWOD	diuretic hormone p	906	5	4.1	149	1	G70400	conserved hypothet
834	5	4.1	138	2	PH1564	Ig heavy chain v r	907	5	4.1	149	2	T09674	ribosomal protein
835	5	4.1	138	2	PH1564	Ig heavy chain v r	908	5	4.1	149	2	D83256	heat-shock protein
836	5	4.1	138	2	T43365	ribosomal protein	909	5	4.1	149	2	F72677	hypothetical prote
837	5	4.1	138	2	S24100	envelope protein -	910	5	4.1	150	2	S72852	hypothetical prote
838	5	4.1	138	2	D71172	hypothetical prote	911	5	4.1	150	2	C86754	prophage pi2 prote
839	5	4.1	138	2	T39043	hypothetical prote	912	5	4.1	150	2	S73725	probable lipoprote
840	5	4.1	138	2	T34049	hypothetical prote	913	5	4.1	150	2	C71297	probable transmem
841	5	4.1	138	2	T04516	hypothetical prote	914	5	4.1	151	1	E65001	hypothetical prote
842	5	4.1	139	2	JX0238	UPglucose 4-epime	915	5	4.1	151	2	T16284	hypothetical prote
843	5	4.1	139	2	PH1558	Ig heavy chain v r	916	5	4.1	151	2	A96493	hypothetical prote
844	5	4.1	139	2	S43769	cold-regulated pro	917	5	4.1	151	2	A72409	conserved hypothet
845	5	4.1	139	2	S60916	probable membrane	918	5	4.1	152	2	I77327	NADH dehydrogenase
846	5	4.1	139	2	T03372	high mobility grou	919	5	4.1	152	2	S34819	embryonic abundant
847	5	4.1	140	1	IIMSG1	interleukin-4 prec	920	5	4.1	152	2	S19388	probable membrane
848	5	4.1	140	2	H71903	hypothetical prote	921	5	4.1	152	2	S64605	hypothetical prote
849	5	4.1	140	2	H82651	hypothetical prote	922	5	4.1	153	1	S17722	H+-transporting AT
850	5	4.1	140	2	G69986	hypothetical prote	923	5	4.1	153	2	S36752	embryonic abundant
851	5	4.1	141	2	S11685	Ig heavy chain v r	924	5	4.1	153	2	S73686	adhesin F1 homolog
852	5	4.1	141	2	I39059	hypothetical prote	925	5	4.1	153	2	T09832	water-stress-induc
853	5	4.1	141	2	C72606	hypothetical prote	926	5	4.1	153	2	S74290	DOM34 protein homo
854	5	4.1	141	2	C71196	hypothetical prote	927	5	4.1	154	2	S20511	superoxide dismuta
855	5	4.1	142	1	S01714	hemoglobin zeta ch	928	5	4.1	154	2	T00556	60S ribosomal prot
856	5	4.1	142	2	B70830	hypothetical prote	929	5	4.1	154	2	T47667	ribosomal L23a-lik
857	5	4.1	142	2	T44478	hypothetical prote	930	5	4.1	154	2	S49250	glycine cleavage s
858	5	4.1	142	2	T45922	probable C2H2-type	931	5	4.1	154	2	E82015	probable DNA trans
859	5	4.1	143	1	S04230	H+-transporting AT	932	5	4.1	154	2	C81819	hypothetical prote
860	5	4.1	143	1	S18241	alpha-amylase inh	933	5	4.1	154	2	T21023	RNA-binding protei
861	5	4.1	143	2	S34069	H+-transporting AT	934	5	4.1	154	2	JC4588	probable ribosomal
862	5	4.1	143	2	S49229	H-protein - Flaver	935	5	4.1	155	2	G72557	conserved hypothet
863	5	4.1	143	2	E89065	molybdopter bios	936	5	4.1	155	2	D83098	hypothetical prote
864	5	4.1	143	2	H71970	hypothetical prote	937	5	4.1	155	2	T24828	glycine decarboxyl
865	5	4.1	143	2	D81751	conserved hypothet	938	5	4.1	156	2	H84764	hypothetical prote
866	5	4.1	143	2	D83148	hypothetical prote	939	5	4.1	156	2	D72473	hypothetical prote
867	5	4.1	143	2	JC5246	allograft inflama	940	5	4.1	156	2	E83227	probable C2H2-type
868	5	4.1	143	2	T20951	hypothetical prote	941	5	4.1	156	2	C84688	hypothetical prote
869	5	4.1	144	1	YMSMCM	macromycin precu	942	5	4.1	156	2	E84861	hypothetical prote
870	5	4.1	144	1	A28123	transcription fact	943	5	4.1	156	2	S22246	transposable retro
871	5	4.1	144	2	PH1563	Ig heavy chain v r	944	5	4.1	156	2	A32795	T-cell translocati
872	5	4.1	144	2	I46642	rearranged T-cell	945	5	4.1	157	2	JC5551	hypothetical prote
873	5	4.1	144	2	F75470	hypothetical prote	946	5	4.1	157	2	S75191	hypothetical prote
874	5	4.1	144	2	H96511	AP2 domain contain	947	5	4.1	157	2	F71906	similar to S-locus
875	5	4.1	144	2	T14796	hypothetical prote	948	5	4.1	157	2	H84638	hypothetical prote
876	5	4.1	145	2	D81366	probable ribose 5-	949	5	4.1	157	2	H83807	hypothetical prote
877	5	4.1	145	2	S75219	hypothetical prote	950	5	4.1	158	2	S63140	ribosomal protein
878	5	4.1	145	2	T33139	hypothetical prote	951	5	4.1	158	2	F64607	hypothetical prote
879	5	4.1	145	2	A72804	gp34.1 protein - M	952	5	4.1	158	2	B84588	probable AP2 domai
880	5	4.1	145	2	C72668	hypothetical prote	953	5	4.1	158	2	H71229	hypothetical prote
881	5	4.1	145	2	H82110	hypothetical prote	954	5	4.1	159	2	G72249	ribosomal protein
882	5	4.1	145	2	F81338	probable periplasm	955	5	4.1	159	2	A72462	hypothetical prote
883	5	4.1	145	2	F83247	hypothetical prote	956	5	4.1	159	2	H81657	conserved hypothet
884	5	4.1	145	2	D70938	hypothetical prote	957	5	4.1	159	2	T00930	hypothetical prote
885	5	4.1	145	2	H82567	outer membrane pro	958	5	4.1	159	2	D82649	hypothetical prote
886	5	4.1	146	2	A44588	globin - waved whe	959	5	4.1	159	2	F84091	hypothetical prote
887	5	4.1	146	2	A47167	mucin-like endothe	960	5	4.1	159	2	A83295	hypothetical prote
888	5	4.1	146	2	JC4902	ionized calcium bi	961	5	4.1	159	2	S46494	galactoside 2-alph
889	5	4.1	146	2	T38048	very hypothetical	962	5	4.1	160	1	F70351	NADH dehydrogenase
890	5	4.1	146	2	S45128	hypothetical prote	963	5	4.1	160	2	S45632	H+-transporting AT
891	5	4.1	146	2	C72703	hypothetical prote	964	5	4.1	160	2	S47249	gene 1-Sc3 protein
892	5	4.1	147	2	PH1561	Ig heavy chain v r	965	5	4.1	160	2	S30054	major allergen Cor
893	5	4.1	147	2	G86749	conserved hypothet	966	5	4.1	160	2	S30055	major allergen Cor
894	5	4.1	147	2	G85552	ORF-US441 - Infect	967	5	4.1	160	2	S30056	major allergen Cor
895	5	4.1	147	2	JC7237	receptor-activity-	968	5	4.1	160	2	S30053	major allergen Cor
896	5	4.1	147	2	JC7263	receptor activity	969	5	4.1	160	2	T19458	hypothetical prote
897	5	4.1	147	2	I55617	allograft inflama	970	5	4.1	160	2	F75450	hypothetical prote
898	5	4.1	147	2	H82313	hypothetical prote	971	5	4.1	160	2	C84422	hypothetical prote
899	5	4.1	147	2	T30606	hypothetical prote	972	5	4.1	161	1	USURAL	tubulin alpha chai
900	5	4.1	148	2	G75066	hypothetical prote	973	5	4.1	161	2	S71453	glycine-rich RNA-b
901	5	4.1	148	2	JC5281	sporozoite 60K pro	974	5	4.1	161	2	E71866	hypothetical prote
902	5	4.1	148	2	E81016	ComEA-related prot	975	5	4.1	162	2	E69155	hypothetical prote
903	5	4.1	148	2	C81214	ComEA-related prot	976	5	4.1	162	2	H69896	hypothetical prote
904	5	4.1	148	2	A84636	similar to avrRpt2	977	5	4.1	162	2	D96581	hypothetical prote
905	5	4.1	148	2	H83054	suppressor protein	978	5	4.1	162	2	C75497	hypothetical prote

979 5 4.1 163 2 C71977 lipoprotein signal
980 5 4.1 163 2 S55278 translation initia
981 5 4.1 163 2 G72639 hypothetical prote
982 5 4.1 163 2 A71768 T-cell receptor ze
983 5 4.1 163 2 E72473 probable thiorodox
984 5 4.1 164 1 NWU03 2S albumin 3 precu
985 5 4.1 164 2 A40104 T-cell receptor CD
986 5 4.1 164 2 T47547 hypothetical prote
987 5 4.1 164 2 T26952 hypothetical prote
988 5 4.1 164 2 S27529 hypothetical prote
989 5 4.1 165 1 G55079 hypothetical 19.3
990 5 4.1 165 2 A36237 melanin-concentrat
991 5 4.1 165 2 G84767 glycine decarboxyl
992 5 4.1 165 2 S50195 oleosin - rape
993 5 4.1 165 2 S35195 hypothetical prote
994 5 4.1 165 2 G85951 hypothetical prote
995 5 4.1 165 2 A39617 DNA-damage-inducib
996 5 4.1 165 2 F72345 hypothetical prote
997 5 4.1 165 2 T01421 pistil extensin-li
998 5 4.1 166 2 A86450 hypothetical prote
999 5 4.1 166 2 JC4664 T-cell receptor ze
1000 5 4.1 166 2 I46424 T-cell surface gly

ALIGNMENTS

RESULT 1
A43779
neurokinin B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 16-Jul-1999
C:Accession: A43779
R:Bonner, T.I.; Affolter, H.U.; Young, A.C.; Young III, W.S.
Brain Res. Mol. Brain Res. 2, 243-249, 1987
A:Title: A cDNA encoding the precursor of the rat neuropeptide, neurokinin B.
A:Reference number: A43779
A:Accession: A43779
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <BON>
A:Cross-references: GB:M16410; GB:M35607; NID:g205724; PIDN:AAA41711.1; PID:g205725
C:Superfamily: neurokinin B precursor
C:Keywords: neuropeptide

Query Match 8.3%; Score 10; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
| | | | | | | | | |
DB 80 KRDHDFVVG 89

RESULT 2
I65342
tachykinin B precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I65342
R:Kako, K.; Muneke, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A:Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and B.
A:Reference number: I52526
A:Accession: I65342
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-116 <RES>
A:Cross-references: GB:D14423; NID:g407346; PIDN:BAA03316.1; PID:g407347
C:Genetics:
A:Gene: PPT-B
C:Superfamily: neurokinin B precursor

Query Match 8.3%; Score 10; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
| | | | | | | | | |
DB 80 KRDHDFVVG 89

RESULT 3
A25905
tachykinin B precursor - bovine
N:Alternate names: neuromedin K
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C:Accession: A25905
R:Kotani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986
A:Title: Structure and gene organization of bovine neuromedin K precursor.
A:Reference number: A25905; MUID:86313713
A:Accession: A25905
A:Molecule type: DNA
A:Residues: 1-126 <KOT>
A:Cross-references: GB:M14351; NID:gl63587; PIDN:AAA30723.1; PID:gl63590
C:Superfamily: neurokinin B precursor
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-126/Product: protachykinin B #status predicted <MAT>

Query Match 8.3%; Score 10; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
| | | | | | | | | |
DB 84 KRDHDFVVG 93

RESULT 4
SPFGNK
neuromedin K - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 23-Aug-1996
C:Accession: A01560
R:Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 533-540, 1983
A:Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord
A:Reference number: A01560; MUID:83282812
A:Accession: A01560
A:Molecule type: protein
A:Residues: 1-10 <KAN>
A>Note: the structure of the peptide was confirmed by synthesis
C:Comment: The biological source of this peptide is spinal cord. It stimulates smooth
C:Superfamily: neurokinin B precursor
C:Keywords: amidated carboxyl end; hormone; spinal cord
F:10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 DMHDFVVG 88
| | | | | | | |
DB 1 DMHDFVVG 8

RESULT 5
E75338
DNA gyrase, subunit A - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
A:Accession: E75338
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: E75338
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-812 <WHI>
A:Cross-references: GB:AE002030; GB:AE000513; NID:96459692; PIDN:AAF11467.1; PID:9645969
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1913
A:Map position: 1
C:Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phase T4 DNA topoisomerase C

Query Match 6.6%; Score 8; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 LEGLKAL 64
DB 377 LEGLKAL 384
|||||

RESULT 6
S75133
hypothetical protein slr2101 - Synchocystis sp. (strain PCC 6803)
C:Species: Synchocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75133
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis
S.
A:Reference number: S74322; MUID:97061201
A:Accession: S75133
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143 <KAN>
A:Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAAL7995.1; PID:g165307
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 5.8%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 108 VPSFGIL 114
DB 75 VPSFGIL 81
|||||

RESULT 7
H70733
hypothetical protein Rv2300c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: H70733
R:Colle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: H70733

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-310 <COL>
A:Cross-references: GB:277163; GB:AL123456; NID:g3261610; PIDN:CAB00971.1; PID:e25516
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV2300c

Query Match 5.8%; Score 7; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 DPDLXOL 46
DB 299 DPDLXOL 305
|||||

RESULT 8
T50468
probable maturase [imported] - Neurospora crassa mitochondrion
C:Species: mitochondrion Neurospora crassa
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T50468
R:Morelli, G.; Macino, G.
J. Mol. Biol. 178, 491-507, 1984
A>Title: Two intervening sequences in the ATPase subunit 6 gene of Neurospora crassa:
A:Reference number: 225077; MUID:85033713
A:Accession: T50468

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-366 <MOR>
A:Cross-references: EMBL:X01075; NID:g13109; PIDN:CAA25541.1; PID:g3805929
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Keywords: mitochondrion

Query Match 5.8%; Score 7; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 SLEGLLK 62
DB 178 SLEGLLK 184
|||||

RESULT 9
B82846
succinyl-diaminopimelate desuccinylase XF0116 [imported] - Xylella fastidiosa (strain
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: B82846
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: B82846

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <SIM>
A:Cross-references: GB:AE003865; GB:AE003849; NID:g9104892; PIDN:AAF82929.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrier
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A.; Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0116
C:Superfamily: succinyl-diaminopimelate desuccinylase

Query Match 5.8%; Score 7; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 PDLYQLL 47
|||||||

Db 363 PDLYQLL 369

RESULT 10

E75439 conserved hypothetical protein - Deinococcus radiodurans (strain RL)

C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: E75439

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RL.

A:Reference number: A75250; MUID:20036896

A:Accession: E75439

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <WHI>

A:Cross-references: GB:AE001958; GB:AE000513; NID:g6458805; PIDN:AAF10648.1; PID:g645880

A:Experimental source: strain RL

C:Genetics:

A:Gene: DR1075

A:Map position: 1

C:Superfamily: hypothetical protein slr0882

Query Match 5.8%; Score 7; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLFTAIL 11

|||||||

Db 34 LLFTAIL 40

RESULT 11

C81351 probable UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanine 1

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000

C:Accession: C81351

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; MUID:20150912

A:Accession: C81351

A:Molecule type: DNA

A:Residues: 1-475 <PAR>

A:Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73060.1; PID:g696824

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: murF; Cj0795c

C:Keywords: ligase

Query Match 5.8%; Score 7; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 HSSLEGL 60

|||||||

Db 295 HSSLEGL 301

RESULT 12

E96664

hypothetical protein T12P18.4 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: E96664

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: E96664

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-493 <STO>

A:Cross-references: GB:AE005173; NID:g6358782; PIDN:AAF07363.1; GSPDB:GN00141

C:Genetics:

A:Gene: T12P18.4

A:Map position: 1

C:Superfamily: rubredoxin--NAD+ reductase rubB

Query Match 5.8%; Score 7; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 QLLQRLF 51

|||||||

Db 250 QLLQRLF 256

RESULT 13

C83122

probable aldehyde dehydrogenase PA4189 [imported] - Pseudomonas aeruginosa (strain PA

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83122

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L ; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337

A:Accession: C83122

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-496 <STO>

A:Cross-references: GB:AE004835; GB:AE004091; NID:g9950394; PIDN:AAG07576.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA4189

C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 5.8%; Score 7; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 VVPGGGR 36
|||||
Db 220 VVPGGGR 226

RESULT 14
D83775
hypothetical protein BH1004 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: D83775
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20263314
A:Accession: D83775
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-534 <STO>
A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04723.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1004

Query Match 5.8%; Score 7; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MLLFTAI 10
|||||
Db 87 MLLFTAI 93

RESULT 15
A54372
G protein-coupled receptor kinase (EC 2.7.1.1-) 5 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A54372
R:Premont, R.T.; Koch, W.J.; Inglesse, J.; Lefkowitz, R.J.
J. Biol. Chem. 269, 6832-6841, 1994
A:Title: Identification, purification, and characterization of GRK5, a member of the fam
A:Reference number: A54372; MUID:94165084
A:Accession: A54372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <PRE>
A:Cross-references: GB:U01206; NID:g437105; PIDN:AAA17561.1; PID:g437106
C:Superfamily: rhodopsin kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:184-448/Domain: protein kinase homology <KIN>
F:192-200/Region: protein kinase ATP-binding motif

Query Match 5.8%; Score 7; DB 1; Length 590;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LIQLRFLK 52
|||||
Db 550 LIQLRFLK 556

Search completed: May 3, 2002, 12:29:12
Job time: 128 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:28:49 ; Search time 11.8 Seconds
(without alignments)
375.970 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRIMLLFTAILAFSLAQSG.....DVNQNVPSFGILKYPPRAE 121

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	8.3	116	1	TKNK_MOUSE
2	10	8.3	116	1	TKNK_RAT
3	10	8.3	126	1	TKNK_BOVIN
4	8	6.6	10	1	TKNK_PIG
5	8	6.6	3099	1	POLG_PEMVM
6	7	5.8	310	1	YNO0_MYCTU
7	7	5.8	590	1	GRK5_BOVIN
8	7	5.8	590	1	GRK5_HUMAN
9	7	5.8	648	1	CCMF_HAETN
10	7	5.8	792	1	ATX1_MOUSE
11	6	5.0	63	1	HIG2_HUMAN
12	6	5.0	73	1	SAS2_BACME
13	6	5.0	73	1	SAS5_BACME
14	6	5.0	77	1	Y084_TREPA
15	6	5.0	104	1	YJB8_YEAST
16	6	5.0	108	1	VNBP_PVMS
17	6	5.0	108	1	VNBP_PVMR
18	6	5.0	110	1	Y225_METJA
19	6	5.0	113	1	FT22_HUMAN
20	6	5.0	126	1	SPCG_PSESY
21	6	5.0	130	1	FLHE_ECOLI
22	6	5.0	130	1	FLHE_SALTY
23	6	5.0	141	1	HBAB_RANCA
24	6	5.0	152	1	MYG_APTFO
25	6	5.0	153	1	MYG_HALGR
26	6	5.0	153	1	MYG_PHOSI
27	6	5.0	153	1	MYG_PHYCA
28	6	5.0	154	1	RL2B_TORAC
29	6	5.0	155	1	VG05_BPML5
30	6	5.0	156	1	CB20_HUMAN
31	6	5.0	160	1	Y650_TREPA
32	6	5.0	162	1	YD73_METJA
33	6	5.0	163	1	COAD_STRPY
					P55099 mus musculus
					P08435 rattus norv
					P08858 bos taurus
					P01292 sus scrofa
					O56075 p genome po
					Q50665 mycobacteri
					P43249 bos taurus
					P34947 homo sapien
					P45037 haemophilus
					P54254 mus musculus
					Q9Y512 homo sapien
					P10571 bacillus me
					P04835 bacillus me
					O83122 treponema p
					P47070 saccharomyc
					Q01687 potato viru
					P17530 potato viru
					Q60284 methanococc
					O75474 homo sapien
					P95577 pseudomonas
					P76297 escherichia
					P40728 salmonella
					P51465 rana catesb
					P02199 aptenodytes
					P02162 halichoerus
					P30562 phoca sibir
					P02185 physeter ca
					Q07761 nicotiana t
					Q05267 mycobacteri
					P52298 homo sapien
					O83656 treponema p
					Q58768 methanococc
					P58104 streptococc

168	1	COX2_THETH
173	1	TCPA_AMBME
183	1	SIEB_LAMBD
195	1	RAC4_ARATH
196	1	RAC5_ARATH
197	1	RAC1_ARATH
197	1	RAC1_BETVU
201	1	RAC1_PEA
201	1	GLND_SALTY
208	1	Y146_UREPA
209	1	ENTD_ECOLI
212	1	ER21_BOVIN
212	1	ER21_HUMAN
212	1	OSC2_BORBU
220	1	ALKB_CAUCR
227	1	UPP_HA1N1
228	1	ISPD_BACHD
239	1	RIM9_YEAST
240	1	UL20_VZVD
241	1	CL11_HUMAN
241	1	CL11_MOUSE
245	1	FLIP_ECOLI
245	1	FLIP_SALTY
245	1	GSC_CHICK
245	1	OCCM_RHIME
247	1	RS3_CAEEL
253	1	GS2_HUMAN
258	1	FLIP_ERWCA
260	1	IF31_HUMAN
271	1	CF30_MYCTU
281	1	NHOA_HAETN
282	1	LRPR_STRCO
300	1	NUSG_STRCO
303	1	NULM_CABUN
309	1	NUSG_STRGB
312	1	SNAG_HUMAN
327	1	CD1A_HUMAN
328	1	SNAG_BOVIN
330	1	C1B4_CAVPO
331	1	DGAL_HAETN
333	1	C1B1_CAVPO
333	1	CD1B_HUMAN
335	1	CD1D_HUMAN
335	1	RPC5_YEAST
335	1	TRPD_BUCDN
336	1	CD1D_RAT
337	1	ATH2_MOUSE
344	1	M1ZD_BACSU
348	1	GALE_HUMAN
359	1	AG2R_CANFA
359	1	AG2R_MERUN
359	1	AG2R_MOUSE
359	1	AG2R_PIG
359	1	AG2R_RAT
359	1	RECF_DEIRA
360	1	LPXB_HELPJ
360	1	LPXB_HELPY
361	1	APEA_DICDI
363	1	HRCa_AGRU
365	1	YUCL_YEAST
366	1	YOP3_CAEEL
372	1	HMEN_BOMMO
377	1	SHID_CANFA
379	1	CYB_FELCA
379	1	CYB_LORTA
387	1	GAT6_CHICK
388	1	ODPT_HUMAN
393	1	FMT_YEAST
395	1	CGA2_CHICK
398	1	Y4QJ_RHISN
399	1	NTG1_YEAST
399	1	TCR1_ECOLI

P98052	thermus aqu
P50157	ambystoma m
P03762	bacterioph
Q38919	arabidopsis
Q38937	arabidopsis
Q38902	arabidopsis
Q39435	beta vulgar
Q35638	pisum sativ
P23679	salmonella
Q9P828	ureaplasma
P19225	escherichia
P33946	bos taurus
P24390	homo sapien
Q08137	borrelia bu
Q05725	caulobacter
Q9H005	halobacteri
Q9K9F8	bacillus ha
Q04734	saccharomyc
P09290	varicella-z
O00299	homo sapien
Q921q5	mus musculu
P33133	escherichia
P54700	salmonella
P53545	gallus gall
P72296	rhizobium m
P41522	caenorhabdi
P41247	homo sapien
P34200	erwinia car
O75822	homo sapien
O53774	mycobacteri
Q04160	haemophilus
Q00267	salmonella
Q54087	streptococc
P36266	streptomyce
O78700	cabassous u
P52852	streptomyce
Q99747	homo sapien
P06126	homo sapien
P81127	bos taurus
Q9Q2Y9	cavia porce
P44883	haemophilus
Q9Q222	cavia porce
P29016	homo sapien
P15813	homo sapien
P07703	saccharomyc
O68426	buchnera ap
Q63493	rattus norv
P48986	mus musculu
P26935	bacillus su
Q14376	homo sapien
P43240	canis fami
Q35210	meriones un
P29754	mus musculu
P30555	sus scrofa
Q9RVE0	rattus norv
Q9ZKY2	helicobacte
O25537	helicobacte
P51173	dictyosteli
O68443	agrobacteri
Q22695	saccharomyc
Q22695	caenorhabdi
P27609	bombyx mori
P11614	canis fami
P48886	felis silve
Q34952	loris tard
P43693	gallus gall
P29803	homo sapien
P32785	saccharomyc
P43449	gallus gall
P55631	rhizobium s
P31378	saccharomyc
P02982	escherichia

107	6	5.0	402	1	KAS2_STRCM	P41176 streptomyc	180	6	5.0	727	1	GPDM_RAT	P35571 rattus norv
108	6	5.0	421	1	FXJ1_MOUSE	Q61660 mus musculu	181	6	5.0	727	1	YR22_CAEEL	Q09639 caenorhabdi
109	6	5.0	421	1	FXJ1_RAT	Q63247 rattus norv	182	6	5.0	728	1	SPEL_PEA	Q03075 plisum sativ
110	6	5.0	430	1	CLPX_BORBU	O51557 borrelia bu	183	6	5.0	731	1	CATA_HALMA	O59651 halocaula
111	6	5.0	431	1	CIT1_ECOLI	P07661 escherichia	184	6	5.0	738	1	LDLC_HUMAN	O14746 homo sapien
112	6	5.0	434	1	CIT1_SALTY	P24115 salmonella	185	6	5.0	744	1	GYRA_AQUAE	O67108 aquifex aeo
113	6	5.0	435	1	RUBB_CHLRE	Q42693 chlamydomon	186	6	5.0	746	1	CLCS_MOUSE	P51795 homo sapien
114	6	5.0	443	1	YEY2_YEAST	P10356 saccharomyc	187	6	5.0	746	1	CLCS_MOUSE	Q9wvd4 mus musculu
115	6	5.0	454	1	P2CH_HUMAN	P49593 homo sapien	188	6	5.0	746	1	CLCS_RAT	P51796 rattus norv
116	6	5.0	456	1	PUR1_ARCFU	Q29388 archaeoglob	189	6	5.0	748	1	KLH1_HUMAN	Q9nr64 homo sapien
117	6	5.0	459	1	ZPR1_HUMAN	O75312 homo sapien	190	6	5.0	779	1	SRP_DROME	P52172 drosophila
118	6	5.0	459	1	ZPR1_MOUSE	Q62384 mus musculu	191	6	5.0	788	1	PAB5_YEAST	P37254 saccharomyc
119	6	5.0	464	1	L2AM_DROME	P18486 drosophila	192	6	5.0	802	1	PEFC_SALTY	P37868 salmonella
120	6	5.0	470	1	CPBK_MOUSE	Q62397 mus musculu	193	6	5.0	804	1	GYRA_THEMEA	Q33926 thermotoga
121	6	5.0	479	1	SAHH_PLAF7	P50250 plasmodium	194	6	5.0	810	1	SYEF_SYNY3	O74296 synechocyst
122	6	5.0	481	1	CAP_CHLVR	Q01122 chlorohydra	195	6	5.0	812	1	P3K2_SOYBN	P42348 glycine max
123	6	5.0	484	1	DNA4_ZYMMO	Q9s493 zymomonas m	196	6	5.0	814	1	P3K1_SOYBN	P42347 glycine max
124	6	5.0	491	1	CPB1_RAT	P00176 rattus norv	197	6	5.0	824	1	CC27_HUMAN	P30260 homo sapien
125	6	5.0	491	1	CPB2_RAT	P04167 rattus norv	198	6	5.0	824	1	SYL_THEMEA	Q9wy15 thermotoga
126	6	5.0	491	1	CPB4_RABIT	P00178 oryctolagus	199	6	5.0	831	1	DPO1_THEMEA	P30313 thermus aqu
127	6	5.0	491	1	CPB5_RABIT	P12789 oryctolagus	200	6	5.0	832	1	DPO1_THEMEA	P19821 thermus aqu
128	6	5.0	491	1	CPB6_HUMAN	P20813 homo sapien	201	6	5.0	853	1	CNRB_BOVIN	P23439 bos taurus
129	6	5.0	491	1	CPB9_MOUSE	P12790 mus musculu	202	6	5.0	854	1	CNRB_HUMAN	P35913 homo sapien
130	6	5.0	492	1	CPBC_RAT	P33272 rattus norv	203	6	5.0	856	1	CNRB_MOUSE	P23440 mus musculu
131	6	5.0	492	1	CPB1_MOUSE	O55071 mus musculu	204	6	5.0	864	1	GYRA_STRCO	P35895 streptomyc
132	6	5.0	492	1	SESL_HUMAN	Q95965 homo sapien	205	6	5.0	867	1	GLND_KLEPN	P41393 klebsiella
133	6	5.0	492	1	SESL_MOUSE	P58006 mus musculu	206	6	5.0	890	1	BCN5_CLOPE	P08696 clostridium
134	6	5.0	494	1	CPBB_CANFA	P24460 canis famli	207	6	5.0	890	1	GLND_ECOLI	P27249 escherichia
135	6	5.0	500	1	CPBA_MOUSE	P12791 mus musculu	208	6	5.0	895	1	YA54_METJA	O58454 methanococ
136	6	5.0	510	1	FKH_DROME	P14734 drosophila	209	6	5.0	908	1	DPO1_BORBU	O51498 borrelia bu
137	6	5.0	510	1	SYK_SYNY3	P73443 synechocyst	210	6	5.0	932	1	PMS1_HUMAN	P54277 homo sapien
138	6	5.0	512	1	AMT1_DEBOC	P19269 debaryomyc	211	6	5.0	944	1	SUHW_DROME	P08970 drosophila
139	6	5.0	516	1	GUX1_NEUCR	P38676 neurospora	212	6	5.0	989	1	PSD1_CAEEL	Q18115 caenorhabdi
140	6	5.0	526	1	IEG3_HSV7J	P52355 human herpe	213	6	5.0	1005	1	EVG_MOUSE	P57680 mus musculu
141	6	5.0	534	1	LY41_STRCO	O86511 streptomyc	214	6	5.0	1018	1	YK2_CAEEL	P41933 caenorhabdi
142	6	5.0	541	1	CH60_EHREQ	O34191 ehrlchia e	215	6	5.0	1021	1	ATN1_CHICK	P09572 gallus gall
143	6	5.0	541	1	CH62_RHOSH	P95647 rhodobacter	216	6	5.0	1063	1	ELF1_DROME	P13002 drosophila
144	6	5.0	545	1	CH60_BORBU	P27575 borrelia bu	217	6	5.0	1101	1	DIA2_HUMAN	Q60879 homo sapien
145	6	5.0	545	1	CH60_PSEPU	P48216 pseudomonas	218	6	5.0	1197	1	Y4CA_RHISN	P55383 rhizobium s
146	6	5.0	547	1	CH60_BORPE	P48210 bordetella	219	6	5.0	1222	1	YMP3_CAEEL	Q10947 caenorhabdi
147	6	5.0	547	1	CH60_PSEAE	P30718 pseudomonas	220	6	5.0	1230	1	SMC3_YEAST	P47037 saccharomyc
148	6	5.0	547	1	TCPA_TETPY	O15891 tetrahymena	221	6	5.0	1276	1	MDR1_CRIGR	P21448 cricetus
149	6	5.0	550	1	CH60_EHRCH	P42382 ehrlchia c	222	6	5.0	1276	1	MDR2_CRIGR	P21449 cricetus
150	6	5.0	551	1	ASLA_ECOLI	P25549 escherichia	223	6	5.0	1276	1	MDR2_MOUSE	P21440 mus musculu
151	6	5.0	551	1	CH60_COWRU	P48213 cowdria rum	224	6	5.0	1277	1	MDR2_RAT	P43245 rattus norv
152	6	5.0	552	1	CH60_COXBU	P19421 coxiella bu	225	6	5.0	1278	1	MDR2_MOUSE	Q08201 rattus norv
153	6	5.0	552	1	CH60_PSEST	O33500 pseudomonas	226	6	5.0	1381	1	MDR3_CRIGR	P21374 cricetus
154	6	5.0	553	1	YMB8_YEAST	Q04847 saccharomyc	227	6	5.0	1371	1	VCAP_HSVSA	Q00999 herpesvirus
155	6	5.0	554	1	ATRA_STRCO	Q9X300 streptomyc	228	6	5.0	1587	1	TOP2_PENCH	Q09898 penicillium
156	6	5.0	556	1	TCP1_MOUSE	P11984 mus musculu	229	6	5.0	1630	1	ESPL_YEAST	Q03018 saccharomyc
157	6	5.0	556	1	TCP2_MOUSE	P11983 mus musculu	230	6	5.0	1966	1	MYSB_CAEEL	P02566 caenorhabdi
158	6	5.0	556	1	TCPA_CRIGR	P18279 cricetus	231	6	5.0	2131	1	YCF2_SPTOL	P08973 spinacia ol
159	6	5.0	556	1	TCPA_HUMAN	P17987 homo sapien	232	6	5.0	2212	1	RRPL_EBOZM	Q05318 ebola virus
160	6	5.0	556	1	TCPA_RAT	P28480 rattus norv	233	6	5.0	2294	1	YCF2_ARATH	P56786 arabidopsis
161	6	5.0	556	1	TCPA_SCHPO	Q94501 schizosacch	234	6	5.0	2670	1	YAF5_SCHPO	Q10105 schizosacch
162	6	5.0	557	1	TCPA_MONDO	Q9xt06 monodelphis	235	6	5.0	2769	1	THYC_BOVIN	P01267 bos taurus
163	6	5.0	559	1	TCPA_PALFA	Q9w790 paleosuchus	236	6	5.0	3421	1	TEGU_HSVBE	P28955 equine herp
164	6	5.0	559	1	TCPA_YEAST	P12612 saccharomyc	237	6	5.0	4499	1	DYHA_CHLRE	Q39610 chlamydomon
165	6	5.0	565	1	UBPN_HUMAN	Q9uk80 homo sapien	238	6	5.0	4	1	TLP_ACTDE	P81370 actinidia d
166	6	5.0	566	1	UBPN_MOUSE	Q9q216 mus musculu	239	5	4.1	29	1	AP65_CARMA	P82964 carcinus ma
167	6	5.0	570	1	MKS8_HUMAN	Q9npj1 homo sapien	240	5	4.1	30	1	PSAN_CYACA	Q9tix5 cyanidium c
168	6	5.0	570	1	MKS8_MOUSE	P9fj170 mus musculu	241	5	4.1	36	1	RET4_CHICK	P30370 gallus gall
169	6	5.0	575	1	RECJ_ERWCH	P39693 erwinia chr	242	5	4.1	43	1	MTA_COLVI	P27086 colinus vir
170	6	5.0	576	1	GRK6_HUMAN	P43250 homo sapien	243	5	4.1	43	1	MTB_COLVI	P27087 colinus vir
171	6	5.0	576	1	GRK6_MOUSE	O70293 mus musculu	244	5	4.1	44	1	RK32_LYCES	P36493 lycopersico
172	6	5.0	576	1	GRK6_RAT	P97711 rattus norv	245	5	4.1	48	1	RK32_VICFA	P36493 lycopersico
173	6	5.0	628	1	MSLN_HUMAN	Q13421 homo sapien	246	5	4.1	50	1	C555_BACAZ	P23037 bacillus az
174	6	5.0	658	1	DNLJ_MYCPN	P78021 mycoplasma	247	5	4.1	54	1	RK32_TOBAC	P12198 nicotiana t
175	6	5.0	667	1	YFAE_BACSU	P37519 bacillus su	248	5	4.1	56	1	RK32_SPTOL	P27804 spinacia ol
176	6	5.0	695	1	CMC1_DROME	Q9v673 drosophila	249	5	4.1	59	1	RL37_ARCFU	O29387 archaeoglob
177	6	5.0	695	1	YCX7_CHLVS	O20159 chlorella v	250	5	4.1	60	1	YRHL_BRARE	O42366 brachydanio
178	6	5.0	704	1	YBY1_YEAST	P38273 saccharomyc	251	5	4.1	60	1	YRHL_AZOVI	Q44557 azotobacter
179	6	5.0	725	1	VR2A_BPT4	P03690 bacterioph	252	5	4.1	63	1	MT2_COLLI	P15787 columba liv

253	5	4.1	63	1	MT_CHICK	P09576	gallus gall	326	5	4.1	102	1	RS24_AERPE	Q9ycy0	aeropyrum p
254	5	4.1	64	1	Y314_ARCFU	O29931	archaeoglob	327	5	4.1	105	1	YF40_PYRAB	Q9uz84	pyrococcus
255	5	4.1	65	1	Y975_METJA	O58385	methanococc	328	5	4.1	106	1	Y368_METJA	Q57814	methanococc
256	5	4.1	66	1	YA74_ARCFU	O29189	archaeoglob	329	5	4.1	106	1	Y547_RICPR	Q92d03	rickettsia
257	5	4.1	65	1	YCF9_EUGGR	P32095	euglena gra	330	5	4.1	106	1	Y891_YEAST	P38341	saccharomyc
258	5	4.1	68	1	RK32_MARPO	P12196	marchantia	331	5	4.1	106	1	YCPW_PSEA9	P29298	pseudanabae
259	5	4.1	69	1	RK32_PINTH	P41651	pinus thunb	332	5	4.1	107	1	GUAN_CAVPO	P70664	cavia porce
260	5	4.1	70	1	YVAK_VACCC	P20520	vaccinia vi	333	5	4.1	107	1	VLYS_LAMBD	P03705	bacterioph
261	5	4.1	71	1	FBS_MOUSE	Q60791	mus musculu	334	5	4.1	107	1	YK9_YEAST	P53138	saccharomyc
262	5	4.1	74	1	G0N3_ONCMY	P55246	oncorhynch	335	5	4.1	108	1	ATPR_BOVIN	P02721	bos taurus
263	5	4.1	74	1	G0N3_ONCTS	Q92097	oncorhynch	336	5	4.1	108	1	HEMA_IARI5	P18859	homo sapien
264	5	4.1	75	1	VGE_BPPHK	Q38040	bacterioph	337	5	4.1	108	1	Y19_MOUSE	P03450	influenza a
265	5	4.1	77	1	RS9_TOBAC	P49214	nicotiana t	338	5	4.1	108	1	SY19_MOUSE	O70460	mus musculu
266	5	4.1	77	1	VG43_BPML5	Q05255	mycobacteri	339	5	4.1	108	1	VLY1_BPP22	P09962	bacterioph
267	5	4.1	78	1	GVPA_HALME	P23761	halobacteri	340	5	4.1	108	1	YD08_METJA	Q58704	methanococc
268	5	4.1	79	1	AKHD_DROME	P17975	drosophila	341	5	4.1	109	1	SYR_STRPN	Q54869	streptococc
269	5	4.1	79	1	ATP9_ACACA	Q37377	acanthamoeb	342	5	4.1	109	1	YF79_MYCPN	P55201	mycoplasma
270	5	4.1	79	1	ET2_MACFA	Q28470	macaca fasc	343	5	4.1	110	1	RLAM_YEAST	P02400	saccharomyc
271	5	4.1	80	1	PE_RAT	O54842	rattus norv	344	5	4.1	111	1	ARPP_BOVIN	Q28055	bos taurus
272	5	4.1	81	1	ATPL_CLOAB	O08310	clostridium	345	5	4.1	111	1	ARPP_HUMAN	P56211	homo sapien
273	5	4.1	81	1	YQGY_BACSU	P54502	bacillus su	346	5	4.1	111	1	ARPP_MOUSE	P56212	mus musculu
274	5	4.1	81	1	G0N3_ONCMA	P30973	oncorhynch	347	5	4.1	111	1	OL7H_MOUSE	Q60893	mus musculu
275	5	4.1	82	1	G0N3_SALSA	P35629	salmo salar	348	5	4.1	111	1	SC4_SCHCO	P16934	schizophyll
276	5	4.1	82	1	G0N3_SALTR	P45653	salmo trutt	349	5	4.1	111	1	Y546_SANY3	Q55397	synchocyst
277	5	4.1	82	1	RANA_RANPI	P08950	rana pipien	350	5	4.1	111	1	YDR3_SCHPO	O13738	schizosach
278	5	4.1	82	1	RR16_PORPU	P51352	porphyra pu	351	5	4.1	112	1	FLIN_AQUAE	O67495	aquifex aeo
279	5	4.1	83	1	SEEP_RAPSA	P11573	raphanus sa	352	5	4.1	113	1	DAD1_CAEEL	P52872	caenorhabdi
280	5	4.1	84	1	GLRX_PSEAE	Q9hu55	pseudomonas	353	5	4.1	113	1	RAMA_ENTCL	P55922	enterobacte
281	5	4.1	84	1	Y519_METJA	O57939	methanococc	354	5	4.1	113	1	RAMA_KLEPN	Q48413	klebsiella
282	5	4.1	84	1	Y296_HAEIN	P44220	haemophilus	355	5	4.1	114	1	RL19_SALTY	P36240	salmonella
283	5	4.1	86	1	YVAB_VACCC	P20511	vaccinia vi	356	5	4.1	114	1	SMSA_CARAU	Q9ygh5	carassius a
284	5	4.1	87	1	BXBA_BOMMO	Q17194	bombyx mori	357	5	4.1	114	1	YFEC_ECOLI	P27239	escherichia
285	5	4.1	87	1	RS21_NEUCR	O93798	neurospora	358	5	4.1	114	1	YGI3_BACTU	P10024	bacillus th
286	5	4.1	88	1	RL31_SULSO	P58190	sulfolobus	359	5	4.1	115	1	MOTI_BOVIN	O62820	bos taurus
287	5	4.1	89	1	G0N3_PORNO	P51922	porichthys	360	5	4.1	115	1	MOTI_HUMAN	P12872	homo sapien
288	5	4.1	90	1	DBHA_AERHY	Q91a96	aeromonas h	361	5	4.1	115	1	MOTI_MACMU	O18811	macaca mula
289	5	4.1	90	1	G0N3_DICLA	Q91a09	dicentrarch	362	5	4.1	115	1	MOTI_SHEEP	O18845	ovis aries
290	5	4.1	90	1	G0N3_HAPBU	P45652	haplochromi	363	5	4.1	115	1	PSBW_PORPU	P51347	porphyra pu
291	5	4.1	90	1	G0N3_PAGMA	P51921	pagrus maj	364	5	4.1	115	1	RL19_HAEIN	P44357	haemophilus
292	5	4.1	90	1	G0N3_SPAAU	P51923	sparus aur	365	5	4.1	115	1	RL20_BORBU	O51206	borrelia bu
293	5	4.1	91	1	EMB5_MAIZE	P46517	zea mays (m	366	5	4.1	115	1	SMS1_PROAN	Q9W7f0	protopterus
294	5	4.1	91	1	EML_PICGL	Q40864	picea glauc	367	5	4.1	116	1	MOTI_FELCA	Q9xse2	felis silve
295	5	4.1	92	1	EM6_ARATH	O02973	arabidopsis	368	5	4.1	116	1	Y157_AQUAE	O67709	aquifex aeo
296	5	4.1	92	1	EMB1_DAUCA	P17639	daucus caro	369	5	4.1	118	1	LTP5_ARATH	Q9xf57	arabidopsis
297	5	4.1	92	1	G0N1_CHICK	P37042	gallus gall	370	5	4.1	118	1	YGLX_YEAST	P53231	saccharomyc
298	5	4.1	92	1	LE10_HELAN	P46514	helianthus	371	5	4.1	120	1	LIPB_PROHO	Q51854	prochloroth
299	5	4.1	92	1	MOTI_HORSE	O46617	equus cabal	372	5	4.1	120	1	NU3C_WHEAT	P26303	tritium ae
300	5	4.1	92	1	PTSO_VIBCH	Q9kp46	vibrio chol	373	5	4.1	120	1	RET3_CHICK	P40220	gallus gall
301	5	4.1	93	1	EM1_WHEAT	P04568	tritium ae	374	5	4.1	120	1	VGB_BPG4	P03634	bacterioph
302	5	4.1	93	1	EM3_WHEAT	Q08000	tritium ae	375	5	4.1	121	1	SRI4_ARATH	O04421	arabidopsis
303	5	4.1	93	1	EM4_WHEAT	P2755	tritium ae	376	5	4.1	122	1	Y16A_UREPA	Q9pqx8	ureaplasma
304	5	4.1	93	1	GATC_HELPJ	Q92km6	helicobacte	377	5	4.1	122	1	YJ16_YEAST	P47028	saccharomyc
305	5	4.1	93	1	GATC_HELPJ	O25626	helicobacte	378	5	4.1	123	1	YXG6_YEAST	P53077	saccharomyc
306	5	4.1	93	1	L19A_HORVU	Q05190	hordeum vul	379	5	4.1	124	1	COX4_SAISS	O46582	saimiri sci
307	5	4.1	93	1	L19B_HORVU	P46532	hordeum vul	380	5	4.1	125	1	LECC_POLMI	P16108	polyandroca
308	5	4.1	93	1	Y292_METJA	Q57740	methanococc	381	5	4.1	125	1	NEUM_LBUFA	P08162	bufo japoni
309	5	4.1	93	1	Y008_BPHPI	P51709	bacterioph	382	5	4.1	125	1	YBAN_ECOLI	P45808	escherichia
310	5	4.1	94	1	EM2_WHEAT	P22701	tritium ae	383	5	4.1	125	1	YM88_MYCTU	Q50677	mycobacteri
311	5	4.1	94	1	G0N3_CARAU	P51917	carassius a	384	5	4.1	126	1	MSP2_ASCSU	P27440	ascaris suu
312	5	4.1	94	1	G0N3_RUTRU	Q92106	rutilus rut	385	5	4.1	126	1	WN72_EPTST	P28123	epitretus
313	5	4.1	94	1	N18M_NEUCR	Q07842	neurospora	386	5	4.1	127	1	YBBA_BACSU	P55192	bacillus su
314	5	4.1	95	1	EMPI_ORYSA	P46520	oryza sativ	387	5	4.1	128	1	AR21_ENTHI	O15604	chaetomoeba h
315	5	4.1	96	1	Y1B3_CLOAB	P34159	clostridium	388	5	4.1	128	1	PHE3_CHRSP	Q00433	chromonas
316	5	4.1	97	1	YQ1H_BACSU	P40770	bacillus su	389	5	4.1	129	1	NKL_PIG	Q29075	sus scrofa
317	5	4.1	99	1	YD60_METJA	Q58755	methanococc	390	5	4.1	129	1	TKN1_HUMAN	P20366	homo sapien
318	5	4.1	100	1	URE3_ECOLI	Q03282	escherichia	391	5	4.1	130	1	TKN1_BOVIN	P01289	bos taurus
319	5	4.1	100	1	URE3_KLEAE	P18316	klebsiella	392	5	4.1	130	1	TKN1_MESAU	Q60541	mesocricetu
320	5	4.1	100	1	URE3_KLEPN	O02943	klebsiella	393	5	4.1	130	1	TKN1_MOUSE	P41539	mus musculu
321	5	4.1	100	1	URE3_PROMI	P17088	proteus mir	394	5	4.1	130	1	TKN1_RAT	P06767	rattus norv
322	5	4.1	100	1	URE3_PROVU	P16124	proteus vul	395	5	4.1	131	1	BACH_HALAR	Q53461	haloarcula
323	5	4.1	101	1	PRG1_SALTY	P41785	salmonella	396	5	4.1	131	1	SODN_STRCO	P80735	streptomyce
324	5	4.1	102	1	LE19_GOSHI	P09443	gossypium h	397	5	4.1	131	1	ULC7_HCMVA	P16771	human cytom
325	5	4.1	102	1	MGN_ORYSA	P49030	oryza sativ	398	5	4.1	131	1	Y356_VIBCH	Q9kv02	vibrio chol

691	5	4.1	233	1	RECO_PSEAE	Q9xcx7 pseudomonas	764	5	4.1	253	1	CIOB_RAT	P31721 rattus norv
692	5	4.1	233	1	RS3_BUCAI	P57585 buchnera ap	765	5	4.1	253	1	TA4_EIMTE	P13399 elmeria ten
693	5	4.1	233	1	TL16_ARATH	O22773 arabidopsis	766	5	4.1	253	1	TRPA_LACLA	Q01997 lactococcus
694	5	4.1	234	1	AOX2_AERPE	Q9vdx7 aeropyrum p	767	5	4.1	254	1	KO7_CAEEL	P34295 caenorhabdi
695	5	4.1	234	1	GCH1_SYN3	Q55759 synechocyst	768	5	4.1	255	1	DLX1_MOUSE	Q64317 mus musculu
696	5	4.1	234	1	TFD1_ALCEU	P42428 alcaligenes	769	5	4.1	255	1	QCRC_BACSU	P46913 bacillus su
697	5	4.1	234	1	YMF1_ECOLI	P75968 escherichia	770	5	4.1	256	1	HC3_MOUSE	Q02591 mus musculu
698	5	4.1	235	1	RGS1_MOUSE	Q99pg4 mus musculu	771	5	4.1	256	1	HM34_CAEEL	Q04165 caenorhabdi
699	5	4.1	236	1	H1S4_RHOCA	O30725 rhodobacter	772	5	4.1	256	1	HYPB_HYPLI	P35588 hypoderma l
700	5	4.1	236	1	NUOC_MYCTU	P95179 mycobacteri	773	5	4.1	256	1	PDX3_HUMAN	P30048 homo sapien
701	5	4.1	236	1	TENA_BACSU	P25052 bacillus su	774	5	4.1	256	1	UPPS_BACHD	Q9ka67 bacillus ba
702	5	4.1	237	1	H1S4_METJA	Q58927 methanococc	775	5	4.1	256	1	VATD_YEAST	P32610 saccharomyc
703	5	4.1	237	1	LPXH_HAEIN	P44046 haemophilus	776	5	4.1	256	1	YQEU_BACSU	P54461 bacillus su
704	5	4.1	237	1	R33A_HUMAN	Q14088 homo sapien	777	5	4.1	257	1	FMB1_BACNO	P17834 bacteroides
705	5	4.1	237	1	R33A_MOUSE	P97950 mus musculu	778	5	4.1	257	1	FMBX_BACNO	P27905 bacteroides
706	5	4.1	237	1	VE39_MYCPN	P75339 mycoplasma	779	5	4.1	257	1	ICBE_MOUSE	O89094 mus musculu
707	5	4.1	238	1	CHV1_RHISN	P50351 rhizobium s	780	5	4.1	257	1	NOCP_AGRTU	P35116 agrobacteri
708	5	4.1	238	1	YATF_RHISN	P55660 rhizobium s	781	5	4.1	257	1	VATD_CAEEL	P34462 caenorhabdi
709	5	4.1	239	1	CENB_SHEEP	P94511 ovis aries	782	5	4.1	257	1	YGB5_BPNF	P11186 bacterioph
710	5	4.1	239	1	RNC_HELPJ	Q921h2 helicobacte	783	5	4.1	257	1	YGBF_BACSU	O34447 bacillus su
711	5	4.1	239	1	SFSA_RHIME	O87322 rhizobium m	784	5	4.1	257	1	YGIE_ECOLI	P24198 escherichia
712	5	4.1	239	1	YOCB_HAEIN	P44197 haemophilus	785	5	4.1	258	1	C4BB_RAT	Q63515 rattus norv
713	5	4.1	240	1	CHV1_RHIME	P50350 rhizobium m	786	5	4.1	258	1	TEXF_RHILT	P42728 rhizobium l
714	5	4.1	240	1	COLJ_ONCM7	Q04618 oncorhynch	787	5	4.1	258	1	YAAA_ECOLI	P11288 escherichia
715	5	4.1	240	1	KTHY_ASFB7	P42490 african swi	788	5	4.1	258	1	DEOC_ECOLI	P00882 escherichia
716	5	4.1	240	1	US19_HCMVA	P09725 human cytom	789	5	4.1	259	1	YZ24_METJA	Q60283 methanococ
717	5	4.1	241	1	CTR3_YEAST	Q06686 saccharomyc	790	5	4.1	260	1	NQRC_PASMU	O9c1a9 pasteurella
718	5	4.1	241	1	DCOP_THETH	P96076 thermus aqu	791	5	4.1	261	1	RFA4_HUMAN	Q13156 homo sapien
719	5	4.1	241	1	PSNA_SULSO	O9uxc6 sulfolobus	792	5	4.1	261	1	RNG7_MOUSE	P35737 mus musculu
720	5	4.1	241	1	TRUA_AQUAE	O68953 aquifex aeo	793	5	4.1	261	1	TAM_MYCTU	O53698 mycobacteri
721	5	4.1	241	1	Y26A_HAEIN	O86224 haemophilus	794	5	4.1	262	1	ATF6_ALLAR	P50363 allomyces a
722	5	4.1	242	1	HAP5_YEAST	Q02516 saccharomyc	795	5	4.1	262	1	ATP6_ALIMA	P50364 allomyces m
723	5	4.1	242	1	YZ2T_AGRVI	Q49537 mycoplasma	796	5	4.1	262	1	GDA1_WHEAT	P04721 triticum ae
724	5	4.1	243	1	VLPE_MYCHR	Q94537 mycoplasma	797	5	4.1	262	1	T2M1_MORSP	P11405 moraxella s
725	5	4.1	243	1	YH57_YEAST	P38833 saccharomyc	798	5	4.1	262	1	ZNUB_BUCAI	P57402 buchnera ap
726	5	4.1	244	1	COBI_PSEDE	P21639 pseudomonas	799	5	4.1	263	1	GP3D_CHLTR	P10557 chlamydia t
727	5	4.1	244	1	LPRA_MYCTU	Q11049 mycobacteri	800	5	4.1	263	1	SUMT_SYN3	Q55749 synechocyst
728	5	4.1	244	1	NQRC_HAEIN	P43957 haemophilus	801	5	4.1	264	1	GP3D_CHLMO	Q46439 chlamydia m
729	5	4.1	244	1	OSL3_ARATH	P50700 arabidopsis	802	5	4.1	264	1	H1S4_SCHPO	Q10184 schizosacch
730	5	4.1	244	1	T2FC_YEAST	P35189 saccharomyc	803	5	4.1	264	1	YBAP_ECOLI	P77301 escherichia
731	5	4.1	245	1	143F_HUMAN	Q04917 homo sapien	804	5	4.1	265	1	COX3_AEGCO	Q36952 aegilops co
732	5	4.1	245	1	143F_MOUSE	P11576 mus musculu	805	5	4.1	265	1	COX3_HELAN	P32808 helianthus
733	5	4.1	245	1	PSA2_SCHPO	O94579 schizosacch	806	5	4.1	265	1	COX3_MAIZE	P09138 zea mays (m
734	5	4.1	245	1	SRA5_CAEEL	Q09207 caenorhabdi	807	5	4.1	265	1	COX3_OENBE	P08745 oenothera b
735	5	4.1	245	1	UL51_HSVB	P28961 equine herp	808	5	4.1	265	1	COX3_ORYSA	P14852 oryza sativ
736	5	4.1	245	1	YABS_BACSU	P37561 bacillus su	809	5	4.1	265	1	COX3_SOYBN	P14853 glycine max
737	5	4.1	245	1	YH77_ARCFU	O28497 archaeoglob	810	5	4.1	265	1	MYO2_VICFA	Q03227 vicia faba
738	5	4.1	246	1	VAD1_DROME	Q9v7d2 drosophila	811	5	4.1	265	1	MYO2_LYCES	P54927 lycopersico
739	5	4.1	246	1	VATD_MANSE	Q9u0s4 manduca sex	812	5	4.1	265	1	SYNP_RAT	P22831 rattus norv
740	5	4.1	247	1	C21U_HUMAN	Q9ufm2 homo sapien	813	5	4.1	265	1	YCD4_YEAST	P25369 saccharomyc
741	5	4.1	247	1	C561_XENLA	Q91577 xenopus lae	814	5	4.1	265	1	YPR5_ECOLI	P22394 escherichia
742	5	4.1	247	1	PMGY_MYCLE	P53531 mycobacteri	815	5	4.1	266	1	HMUV_YERPE	Q56993 yersinia pe
743	5	4.1	247	1	TONB_SERMA	P26185 serratia ma	816	5	4.1	266	1	TRP1_CVACA	Q9t1w8 cyanidium c
744	5	4.1	247	1	VATD_BOVIN	P39942 bos taurus	817	5	4.1	266	1	Y032_TREPA	O83075 treponema p
745	5	4.1	247	1	VATD_HUMAN	Q9y5k8 homo sapien	818	5	4.1	267	1	DCOP_PICST	P49434 pichia stip
746	5	4.1	247	1	VATD_MOUSE	P57746 mus musculu	819	5	4.1	267	1	DCOP_YEAST	P03962 saccharomyc
747	5	4.1	247	1	VATD_RABIT	Q97755 oryctolagus	820	5	4.1	267	1	FBOL_GALME	Q26427 gallieria me
748	5	4.1	249	1	FUCK_HAEIN	P44780 haemophilus	821	5	4.1	267	1	VATD_CANAL	P87220 candida alb
749	5	4.1	249	1	HMX1_CHICK	P28361 gallus gall	822	5	4.1	267	1	VNST_SFSV	P12792 sandfly fev
750	5	4.1	249	1	PSB1_BACSU	P40802 bacillus su	823	5	4.1	267	1	Y89Q_AQUAE	O67039 aquifex aeo
751	5	4.1	249	1	PSB1_HUMAN	Q06323 h proteasom	824	5	4.1	268	1	EXOR_RHIME	O52926 rhizobium m
752	5	4.1	249	1	PSB1_MACFA	P58238 macaca fasc	825	5	4.1	268	1	THIM_ARCFU	Q28204 archaeoglob
753	5	4.1	249	1	PSB1_MOUSE	P97371 mus musculu	826	5	4.1	268	1	TRPA_PASMU	P57854 pasteurella
754	5	4.1	249	1	PSB1_RAT	Q63797 rattus norv	827	5	4.1	269	1	AGAR_ECOLI	P42902 escherichia
755	5	4.1	249	1	VAD2_DROME	Q9nef6 drosophila	828	5	4.1	269	1	RFAZ_SALTY	P26473 salmonella
756	5	4.1	249	1	YC23_CVACA	O19904 cyanidium c	829	5	4.1	269	1	VI03_VACCC	P20499 vaccinia vi
757	5	4.1	250	1	PSA4_SFIOL	P52427 spinacia ol	830	5	4.1	269	1	VI03_VACCV	P12923 vaccinia vi
758	5	4.1	250	1	QCRC_BACST	Q45659 bacillus st	831	5	4.1	269	1	YH93_AQUAE	P33000 variola vir
759	5	4.1	250	1	Y028_RICPR	O05972 rickettsia	832	5	4.1	270	1	HIS7_ARATH	O67862 aquifex aeo
760	5	4.1	251	1	TATC_RICPR	Q9zcg6 rickettsia	833	5	4.1	270	1	ISPD_STRCO	P34047 arabidopsis
761	5	4.1	251	1	UPPS_ANASQ	Q9zej7 anabaena sp	834	5	4.1	270	1	RA25_SCHPO	Q910q8 streptomyce
762	5	4.1	252	1	GSC_HUMAN	P56915 homo sapien	835	5	4.1	270	1	TRUA_ECOLI	P42657 schizosacch
763	5	4.1	253	1	CIOB_MOUSE	P14106 mus musculu	836	5	4.1	270	1		P07649 escherichia

837	5	4.1	270	1	VMT1_DHV11	Q01479	dhori virus	910	5	4.1	291	1	SIX2_HUMAN	Q9npc8	homo sapien
838	5	4.1	271	1	YE53_AQUAE	O67438	aquifex aeo	911	5	4.1	291	1	T2EB_HUMAN	P14984	homo sapien
839	5	4.1	271	1	ECE1_CANAL	O07730	candida alb	912	5	4.1	292	1	NIFM_AZOVI	P14980	azotobacter
840	5	4.1	271	1	YK04_STRGO	Q9f305	streptomyce	913	5	4.1	292	1	V761_TREPA	O83742	treponema p
841	5	4.1	271	1	YM35_MYCTU	Q10517	mycobacteri	914	5	4.1	293	1	CDSA_SVNY3	P73448	s phosphati
842	5	4.1	272	1	LY55_YEAST	P50113	saccharomyc	915	5	4.1	293	1	COAT_PVSP	P16653	potato viru
843	5	4.1	273	1	TRY6_ANOGA	P35040	anopheles g	916	5	4.1	293	1	GLPO_BACSU	P37965	bacillus su
844	5	4.1	273	1	TRO_COTJA	Q08410	coturnix co	917	5	4.1	293	1	NIFH_AZOB	P17303	azospirillu
845	5	4.1	274	1	BAG1_HUMAN	Q99933	homo sapien	918	5	4.1	293	1	NIFH_AZOB	P23119	azotobacter
846	5	4.1	274	1	RS2_AQUAE	O67055	aquifex aeo	919	5	4.1	294	1	NIFM_AZOH	P33178	anabaena sp
847	5	4.1	275	1	DHPS_HAEIN	P43776	haemophilus	920	5	4.1	294	1	NIFH_BRAJA	P06117	bradyrhizob
848	5	4.1	275	1	NUEL_RHIME	P58909	rhizobium m	921	5	4.1	294	1	NIFH_BRASP	P00463	mycorrhizob
849	5	4.1	275	1	UL11_HCMVA	P16721	human cytom	922	5	4.1	294	1	Y237_MPCPN	P75455	mycoplasma
850	5	4.1	275	1	UL34_HSVB	P28954	equine herp	923	5	4.1	294	1	YOGI_BACSU	P46340	bacillus su
851	5	4.1	276	1	BACH_HALHP	Q48315	halobacteri	924	5	4.1	295	1	ISPA_HAEIN	P45204	haemophilus
852	5	4.1	276	1	BACH_HALHS	Q48314	halobacteri	925	5	4.1	295	1	NIFL_RHOA	P08718	rhodospiril
853	5	4.1	276	1	BACH_HALVA	P94853	haloatricula	926	5	4.1	295	1	NIFH_RHOU	P22921	rhodospiril
854	5	4.1	276	1	COX2_HUMAN	O9v6n1	homo sapien	927	5	4.1	296	1	CC2_DICDI	P34112	dictyostell
855	5	4.1	276	1	PANC_HELPY	P58061	helicobacte	928	5	4.1	296	1	FTSX_BACSU	O34876	bacillus su
856	5	4.1	276	1	GPT_HAPXE	O42154	haplochromi	929	5	4.1	296	1	NIFL_AZOC	P26751	azorhizobi
857	5	4.1	277	1	TRPC_PSEPU	P20578	pseudomonas	930	5	4.1	296	1	NIF2_AZOC	P26252	azorhizobi
858	5	4.1	277	1	PHZC_PSECL	Q51520	pseudomonas	931	5	4.1	296	1	NIFH_PLEBO	Q00240	plectonema
859	5	4.1	278	1	PHZF_PSEFL	Q51792	pseudomonas	932	5	4.1	296	1	NIFH_RHISN	P19068	rhizobium s
860	5	4.1	278	1	TPPA_HUMAN	P49638	homo sapien	933	5	4.1	296	1	PSTA_ECOLI	P07654	escherichia
861	5	4.1	278	1	TPPA_RAT	P41034	rattus norv	934	5	4.1	296	1	SIX2_MOUSE	O62332	mus musculu
862	5	4.1	278	1	VG48_HSV11	Q00112	ictaluriid h	935	5	4.1	297	1	NIFH_RHIT	P00462	rhizobium e
863	5	4.1	278	1	VPX4_BRUB	P54080	brucella ab	936	5	4.1	297	1	NIFH_RHIT	P00461	rhizobium l
864	5	4.1	279	1	LPXA_BRUB	Q92452	pseudomonas	937	5	4.1	297	1	NIFH_RHIME	P00460	rhizobium m
865	5	4.1	280	1	MCDB_PSEPU	P95836	synecococc	938	5	4.1	297	1	VGIG_HRSV4	P27023	human respi
866	5	4.1	280	1	MURC_SVNP7	Q92433	rickettsia	939	5	4.1	297	1	VGIG_HRSV6	P27025	human respi
867	5	4.1	280	1	Y747_RICPR	Q58419	methanococc	940	5	4.1	297	1	VGIG_HRSV7	P27026	human respi
868	5	4.1	281	1	PSTA_METJA	P46571	caenorhabdi	941	5	4.1	298	1	RNH3_CHLPN	Q926j1	chlamydia p
869	5	4.1	281	1	YFPL_BACSU	P46921	bacillus su	942	5	4.1	298	1	VGIG_HRSV5	P27024	human respi
870	5	4.1	282	1	OPAB_BACSU	P45190	haemophilus	943	5	4.1	299	1	CRX_HUMAN	O43186	homo sapien
871	5	4.1	282	1	PSTA_HAEIN	P46571	caenorhabdi	944	5	4.1	299	1	CRX_MOUSE	O54751	mus musculu
872	5	4.1	282	1	SRG2_CAEEL	Q9m81	tupaia para	945	5	4.1	299	1	HEM6_HUMAN	Q92874	homo sapien
873	5	4.1	282	1	VV_TPMV	Q58650	methanococc	946	5	4.1	299	1	HEM6_ECOLI	P36553	escherichia
874	5	4.1	282	1	Y533_METJA	P03242	human adeno	947	5	4.1	299	1	HEM6_SALTY	P33771	salmonella
875	5	4.1	283	1	EXXK_ADE02	P32422	human adeno	948	5	4.1	299	1	NIFH_ANASP	P00457	anabaena sp
876	5	4.1	283	1	INSK_ECOLI	P19769	escherichia	949	5	4.1	299	1	RL5_BONMO	O76190	bombyx mori
877	5	4.1	283	1	LECH_MOUSE	P34927	mus musculu	950	5	4.1	299	1	YHJC_ECOLI	P37641	escherichia
878	5	4.1	283	1	LECH_RAT	Q02706	rattus norv	951	5	4.1	300	1	RP32_AGRU	P50507	agrobacteri
879	5	4.1	283	1	T2AL_RUEGE	Q9khv6	ruegeria ge	952	5	4.1	302	1	MCRI_YEAST	P36060	saccharomyc
880	5	4.1	283	1	V585_BPBO3	Q37889	bacterioph	953	5	4.1	302	1	YBEJ_ECOLI	P37902	escherichia
881	5	4.1	284	1	NIF1_METTL	P25767	methanococc	954	5	4.1	302	1	YET6_YEAST	P40065	saccharomyc
882	5	4.1	284	1	YAGM_ECOLI	P71296	escherichia	955	5	4.1	302	1	ERA_BACHO	O9k452	bacillus ha
883	5	4.1	285	1	LAFT_VIBPA	Q03477	vibrio para	956	5	4.1	304	1	Y687_HAEIN	P71356	haemophilus
884	5	4.1	285	1	PARP_ECOLI	P19071	escherichia	957	5	4.1	305	1	PYRB_SERMA	P19310	serratia ma
885	5	4.1	285	1	Y539_AQUAE	O6818	aquifex aeo	958	5	4.1	305	1	YYAM_BACSU	P37511	bacillus su
886	5	4.1	286	1	GDAO_WHEAT	P02863	tritium ae	959	5	4.1	306	1	CH38_DROME	P07183	drosophila
887	5	4.1	286	1	MEPA_HAEIN	P44566	haemophilus	960	5	4.1	306	1	YL86_CAEEL	P34444	caenorhabdi
888	5	4.1	286	1	RT28_YEAST	P21771	saccharomyc	961	5	4.1	306	1	YQXF_BACSU	P54569	bacillus su
889	5	4.1	286	1	YGBB_EDWTC	O52401	edwardsiell	962	5	4.1	307	1	CIW8_MOUSE	O922t1	mus musculu
890	5	4.1	286	1	YNIA_ECO57	P58065	escherichia	963	5	4.1	307	1	PYRB_HELPJ	Q92m81	helicobacte
891	5	4.1	286	1	YNIA_ECOLI	P77739	escherichia	964	5	4.1	307	1	PYRB_HELPY	O25716	helicobacte
892	5	4.1	287	1	NIFH_FRAAL	P08925	frankia aln	965	5	4.1	307	1	RNHL_YEAST	P53942	saccharomyc
893	5	4.1	287	1	PPCK_SALTY	P41033	salmonella	966	5	4.1	308	1	FTSQ_BARBA	O9x5h9	bartonella
894	5	4.1	287	1	YJWJ_ECOLI	P39409	escherichia	967	5	4.1	308	1	Y31_METJA	Q58437	methanococc
895	5	4.1	288	1	BLC3_PSEAE	P37322	pseudomonas	968	5	4.1	309	1	FSTL_FLABI	P52838	flaveria bi
896	5	4.1	288	1	BLC6_VIBCH	P81781	vibrio chol	969	5	4.1	309	1	IK11_YEAST	P38874	saccharomyc
897	5	4.1	288	1	BLP1_PSEAE	Q03170	pseudomonas	970	5	4.1	309	1	PYRB_VIBS2	P96174	vibrio sp.
898	5	4.1	288	1	HME2_CHICK	P16897	pseudomonas	971	5	4.1	310	1	DOS1_YEAST	P54858	saccharomyc
899	5	4.1	288	1	KPPR_ECOLI	Q05917	gallus gall	972	5	4.1	310	1	LACC_STAAT	P11099	staphylococ
900	5	4.1	289	1	KPPR_ECOLI	P37307	escherichia	973	5	4.1	311	1	DO34_YEAST	P33309	saccharomyc
901	5	4.1	289	1	MTW1_YEAST	P39731	saccharomyc	974	5	4.1	311	1	V311_ASF87	P23163	african swi
902	5	4.1	289	1	RIPS_TRIKI	P24478	trichosan	975	5	4.1	311	1	YXAF_BACSU	Q07835	bacillus su
903	5	4.1	289	1	V510_ARCFU	O23740	archaeoglob	976	5	4.1	312	1	CAH4_BOVIN	Q95323	bos taurus
904	5	4.1	290	1	LECH_HUMAN	P07306	homo sapien	977	5	4.1	312	1	CAH4_HUMAN	P22748	homo sapien
905	5	4.1	290	1	T2M3_METJA	Q58017	methanococc	978	5	4.1	312	1	COAA_VIBCH	Q9kv38	vibrio chol
906	5	4.1	291	1	BACH_NATPH	P15647	natronomona	979	5	4.1	313	1	CIW6_HUMAN	Q9v257	homo sapien
907	5	4.1	291	1	ISPA_MICLU	O66126	micrococc	980	5	4.1	313	1	GD47_WHEAT	P04727	tritium ae
908	5	4.1	291	1	KPPR_ALCEU	P19924	alcaligenes	981	5	4.1	313	1	M2OM_RAT	P97700	rattus norv
909	5	4.1	291	1	KPPR_ALCEU	P19923	alcaligenes	982	5	4.1	313	1	SPBB_STRCL	P37819	streptomyce

983 5 4.1 313 1 TFS2_DROME
 984 5 4.1 313 1 YDCU_ECOLI
 985 5 4.1 314 1 CYF_ODOSI
 986 5 4.1 314 1 TPIC_FRAAN
 987 5 4.1 314 1 YHML_YEAST
 988 5 4.1 315 1 SOL2_YEAST
 989 5 4.1 315 1 SX22_HUMAN
 990 5 4.1 315 1 VN35_ROT11
 991 5 4.1 316 1 KHSE_MYCTU
 992 5 4.1 317 1 TFB3_HALN1
 993 5 4.1 317 1 YG98_MYCLE
 994 5 4.1 318 1 NIA_CHLVU
 995 5 4.1 318 1 NUJM_BALMU
 996 5 4.1 318 1 NUJM_BOVIN
 997 5 4.1 318 1 NUJM_PIG
 998 5 4.1 319 1 AES_ECOLI
 999 5 4.1 319 1 GCP_MYCPN
 1000 5 4.1 319 1 GDA5_WHEAT

ALIGNMENTS

RESULT 1
 ID TKNK_MOUSE STANDARD; PRT; 116 AA.
 AC P55099;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NEUROKININ B PRECURSOR (NEUROMEDIN K) (PREPROTACHYKININ B) (PPT-B).
 GN TAC3 OR NKNB OR TAC2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10990;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Koko K., Muneoka E., Hosaka M., Murakami K., Nakayama K.;
 RT "Cloning and sequence analysis of mouse cDNAs encoding
 preprotachykinin A and B."
 RL Biomed. Res. 14:253-259(1993).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D14423; BAA03316.1; ..
 CC MGD: MGI:98476; Tac2.
 CC InterPro: IPR003635; Neurokinin.
 CC InterPro: IPR002040; Tachykinin.
 CC ProDom: PD020370; Neurokinin; 1.
 CC PROSITE: PS00267; TACHYKININ; 1.
 CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 CC Amidation; Signal.
 CC SIGNAL 1 20 POTENTIAL.
 CC PEPTIDE 82 91 NEUROKININ B.
 CC MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
 CC SEQUENCE 116 AA; 12809 MW; BF6E89373E2031CC CRC64;

Query Match 8.3%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 79 KRDHDFVVG 88
 DB 80 KRDHDFVVG 89
 RESULT 2
 ID TKNK_RAT STANDARD; PRT; 116 AA.
 AC P08435;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NEUROKININ B PRECURSOR (NEUROMEDIN K).
 GN TAC3 OR NKNB OR NKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=88051833; PubMed=3479225;
 RA Bonner T.I., Aifolter H.-U., Young A.C., Young W.S. III;
 RT "A cDNA encoding the precursor of the rat neuropeptide, neurokinin
 B."
 RL Brain Res. 388:243-249(1987).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M16410; AAA41711.1; ..
 CC PIR: A43779; A43779.
 CC InterPro: IPR003635; Neurokinin.
 CC InterPro: IPR002040; Tachykinin.
 CC ProDom: PD020370; Neurokinin; 1.
 CC PROSITE: PS00267; TACHYKININ; 1.
 CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 CC Amidation; Signal.
 CC SIGNAL 1 20 POTENTIAL.
 CC PEPTIDE 82 91 NEUROKININ B.
 CC MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
 CC SEQUENCE 116 AA; 12659 MW; C73EC67F2BAF8C8C CRC64;
 Query Match 8.3%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 79 KRDHDFVVG 88
 DB 80 KRDHDFVVG 89
 RESULT 3
 ID TKNK_BOVIN STANDARD; PRT; 126 AA.
 AC P08856;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NEUROKININ B PRECURSOR (NEUROMEDIN K).
 GN TAC3 OR NKNB OR NKB.

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86313713; PubMed=3462746;
RA Kotani H., Hoshimaru M., Nawa H., Nakanishi S.;
RT "Structure and gene organization of bovine neuromedin K precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:7074-7078(1986).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M14351; AAA30723.1; -
DR EMBL; M14347; AAA30723.1; JOINED.
DR EMBL; M14348; AAA30723.1; JOINED.
DR EMBL; M14349; AAA30723.1; JOINED.
DR EMBL; M14350; AAA30723.1; JOINED.
DR PIR; A25905; A25905.
DR InterPro; IPR003635; Neurokinin.
DR InterPro; IPR002040; Tachykinin.
DR ProDom; PD020370; Neurokinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PEPTIDE 86 95 NEUROKININ B.
FT MOD_RES 95 95 AMIDATION (G-96 PROVIDE AMIDE GROUP).
SQ SEQUENCE 126 AA; 13871 MW; 446EF433498EC059 CRC64;

Query Match 8.3%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVFG 88
DB 84 KRDMHDFVFG 93
[1]

RESULT 4
ID TNKK_PIG STANDARD; PRT; 10 AA.
AC P01292;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NEUROKININ B (NEUROMEDIN K).
GN TAC3 OR NKNB OR NKB.
OS Sus scrofa (Pig), and Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 8406;
[1]
RP SEQUENCE.
RC SPECIES-Pig; TISSUE-Spinal cord;
RX MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
RT spinal cord.";
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).

RNA SEQUENCE.
RC SPECIES=R.ridibunda; TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
CC PIR; A01560; SPPGNK.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CAAL CRC64;

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 DMHDFVFG 88
DB 1 DMHDFVFG 8
[1]

RESULT 5
ID POLG_PEMVM STANDARD; PRT; 3099 AA.
AC O56075;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 6 KDA PROTEIN 2 (6K2);
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN A (NI-A) (NIA)
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.44) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
DE Peanut mottle virus (strain M).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=103926;
[1]
RP SEQUENCE FROM N.A.
RA Flasiński S., Gonzales R.A., Cassidy B.G.;
RT "The complete nucleotide sequence of peanut mottle virus (M strain)
RT genomic RNA.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHD
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- CATALYTIC ACTIVITY: NUCLEAR INCLUSION PROTEIN A HYDROLYSES
CC GLUTAMINYL BONDS, AND ACTIVITY IS FURTHER RESTRICTED BY
CC PREFERENCES FOR THE AMINO ACIDS IN P6'-P1' THAT VARY WITH THE
CC SPECIES OF POTYVIRUS, E.G. GLU-XAA-TYR-XAA-GLN+(SER OR GLY)
CC FOR THE ENZYME FROM TOBACCO ETCH VIRUS. THE NATURAL SUBSTRATE IS
CC THE VIRAL POLYPROTEIN, BUT OTHER PROTEINS AND OLIGOPETIDES
CC CONTAINING THE APPROPRIATE CONSENSUS SEQUENCE ARE ALSO CLEAVED.
CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.

CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF023848; BAB94595.1; -
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001456; Peptidase_C6.
DR InterPro: IPR002540; Poly_P1.
DR InterPro: IPR001592; Poly_coat.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00863; Peptidase_C4; 1.
DR Pfam: PF00851; Peptidase_C6; 1.
DR Pfam: PF00767; Poly_coat; 1.
DR Pfam: PF01577; Poly_P1; 1.
DR Pfam: PF00880; RNA_dep_RNA_pol; 1.
DR PRINTS: PR00966; NIAPOTYPTASE.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 322 N-TERMINAL PROTEIN.
FT CHAIN 323 779 HELPER COMPONENT PROTEINASE.
FT CHAIN 780 1128 PROTEIN P3.
FT CHAIN 1129 1180 6 KDA PROTEIN 1.
FT CHAIN 1181 1814 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1815 1867 6 KDA PROTEIN 2.
FT CHAIN 1868 ? GENOME-LINKED PROTEIN.
FT CHAIN 7 2303 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2304 2821 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2822 3099 COAT PROTEIN.
FT CHAIN 1868 2303 PUTATIVE NUCLEAR INCLUSION PROTEIN A.
FT NP_BIND 1265 1272 ATP (POTENTIAL).
SQ SEQUENCE 3099 AA; 351032 MW; 0D8E9FC7603F0A4B CRC64;

Query Match 6.6%; Score 8; DB 1; Length 3099;
Best Local Similarity 100.0%; Pred.No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 EEVYPGGG 35
Db 546 EEVYPGGG 553

RESULT 6
YN00_MYCTU STANDARD; PRT; 310 AA.
AC Q50655;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 34.4 KDA PROTEIN RV2300C.
GN RV2300C OR MT2357 OR MTCY339.09.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultón J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z71163; CAB00971.1; -
DR EMBL: AB007078; AAK46642.1; -
DR TIGR: MT2357; -
DR Tuberculist: RV2300C; -
DR InterPro: IPR001279; Beta_lactam_met.
DR Pfam: PF00753; lactamase_B; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 310 AA; 34352 MW; 0764F4FA64AB5E51 CRC64;

Query Match 5.8%; Score 7; DB 1; Length 310;
Best Local Similarity 100.0%; Pred.No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 DPDLYQL 46
Db 299 DPDLYQL 305

RESULT 7
GRK5_BOVIN STANDARD; PRT; 590 AA.
ID GRK5_BOVIN
AC P43249;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR KINASE GRK5 (EC 2.7.1.-).
GN GPRK5 OR GRK5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue epithelium;
RX MEDLINE=94165084; PubMed=8120045;
RA Fremont R.T., Koch W.J., Inglesse J., Lefkowitz R.J.;
RT "Identification, purification, and characterization of GRK5, a member
RT of the family of G protein-coupled receptor kinases.";
RL J. Biol. Chem. 269:6832-6841(1994).
CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE ACTIVATED FORMS OF G
CC PROTEIN-COUPLED RECEPTORS.

```
CC CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN LUNG, HEART, RETINA, LINGUAL
CC CC EPIITHELIUM. VERY LITTLE IN BRAIN, LIVER, KIDNEY.
CC CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CC GPRK SUBFAMILY.
CC CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC EMBL: U01206; AAA17561.1;
CC CC HSSP: Q63450; IA06.
CC CC InterPro: IPR000719; Euk_pkinase.
CC CC InterPro: IPR000239; GPCR_kinase.
CC CC InterPro: IPR000961; Pkinase_C.
CC CC InterPro: IPR000342; RGS.
CC CC InterPro: IPR002290; Ser_thr_kin_actsite.
CC CC Pfam: PF00069; pkinase; 1.
CC CC Pfam: PF00615; RGS; 1.
CC CC PRINTS: PR00717; GPCR_KINASE.
CC CC SMART: SM00315; RGS; 1.
CC CC SMART: SM00133; S_TK_X; 1.
CC CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC CC PROSITE: PS0132; RGS; 1.
CC CC Transferrase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 1 185 N-TERMINAL.
FT DOMAIN 186 448 PROTEIN KINASE.
FT DOMAIN 449 590 C-TERMINAL.
FT NP_BIND 53 171 RGS.
FT BINDING 192 200 ATP (BY SIMILARITY).
FT ACT_SITE 215 311 ATP (BY SIMILARITY).
FT ACT_SITE 311 311 BY SIMILARITY.
FT MOD_RES 484 484 PHOSPHORYLATION (AUTO-).
FT MOD_RES 485 485 PHOSPHORYLATION (AUTO-).
SQ SEQUENCE 590 AA; 67888 MW; E8F353697D8BA6E2 CRC64;

Query Match 5.8%; Score 7; DB 1; Length 590;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LLQRLFK 52
DB 550 LLQRLFK 556

RESULT 8
GRK5_HUMAN
ID GRK5_HUMAN STANDARD; PRT; 590 AA.
AC P34947.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR KINASE GRK5 (EC 2.7.1.-).
GN GRK5 OR GRK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93296183; PubMed=7685906;
RA Kunapuli P., Benovic J.L.;
RT "Cloning and expression of GRK5: a member of the G protein-coupled
RT receptor kinase family."
```

```
RL Proc. Natl. Acad. Sci. U.S.A. 90:5588-5592(1993).
CC CC -!- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE ACTIVATED FORMS OF G
CC CC PROTEIN-COUPLED RECEPTORS.
CC CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN HEART, PLACENTA, LUNG >
CC CC SKELETAL MUSCLE > BRAIN, LIVER, PANCREAS > KIDNEY.
CC CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CC GPRK SUBFAMILY.
CC CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC EMBL: L15388; AAA58620.1;
CC CC HSSP: Q63450; IA06.
CC CC MIM: 600870;
CC CC InterPro: IPR000719; Euk_pkinase.
CC CC InterPro: IPR000239; GPCR_kinase.
CC CC InterPro: IPR000961; Pkinase_C.
CC CC InterPro: IPR000342; RGS.
CC CC InterPro: IPR002290; Ser_thr_kin_actsite.
CC CC Pfam: PF00069; pkinase; 1.
CC CC Pfam: PF00615; RGS; 1.
CC CC PRINTS: PR00717; GPCR_KINASE.
CC CC SMART: SM00315; RGS; 1.
CC CC SMART: SM00220; S_TK_X; 1.
CC CC SMART: SM00133; S_TK_X; 1.
CC CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC CC PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC CC PROSITE: PS0132; RGS; 1.
CC CC Transferrase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 1 185 N-TERMINAL.
FT DOMAIN 186 448 PROTEIN KINASE.
FT DOMAIN 449 590 C-TERMINAL.
FT NP_BIND 53 171 RGS.
FT BINDING 192 200 ATP (BY SIMILARITY).
FT BINDING 215 311 ATP (BY SIMILARITY).
FT ACT_SITE 311 311 BY SIMILARITY.
FT MOD_RES 484 484 PHOSPHORYLATION (AUTO-).
FT MOD_RES 485 485 PHOSPHORYLATION (AUTO-).
SQ SEQUENCE 590 AA; 67786 MW; D363567ECFF5CF21 CRC64;

Query Match 5.8%; Score 7; DB 1; Length 590;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LLQRLFK 52
DB 550 LLQRLFK 556

RESULT 9
CCMF_HAEM
ID CCMF_HAEM STANDARD; PRT; 648 AA.
AC P45037.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCMF.
GN CCMF OR H1094.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
```



```
RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georgagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: REQUIRED FOR THE BIOGENESIS OF C-TYPE CYTOCHROMES.
CC -1- POSSIBLE SUBUNIT OF A HEME LYASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLI/NRFE/CCSA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U32789; AAC22751.1; -
CC TIGR: H11094; -
CC InterPro: IPR002541; CytC_asm.
CC InterPro: IPR003567; CytC_blog.
CC Pfam: PF01578; CytC_asm; 1
KW Cytochrome c-type biogenesis; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 211 231 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
FT TRANSMEM 312 332 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 394 414 POTENTIAL.
FT TRANSMEM 424 444 POTENTIAL.
FT TRANSMEM 448 468 POTENTIAL.
FT TRANSMEM 490 510 POTENTIAL.
FT TRANSMEM 616 636 POTENTIAL.
SQ SEQUENCE 648 AA; 72353 MW; ABE434B80F4B92B6 CRC64;

Query Match 5.8%; Score 7; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AILAFSL 15
DB 280 AILAFSL 286
|||||||

RESULT 10
ATX1_MOUSE
ID ATX1_MOUSE STANDARD; PRT; 792 AA.
AC P54254;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN).
GN SCAL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Brain, Thymus, and Retina;
RX MEDLINE=96381424; PubMed=8789437;
RA Banfi S., Servadio A., Chung M.-Y., Capozzoli F., Duvick L.A.,
RA Elde R., Zoghbi H.Y., Orr H.T.;
RT "Cloning and developmental expression analysis of the murine homolog
RT of the spinocerebellar ataxia type 1 gene (Scal).";
RL Hum. Mol. Genet. 5:33-40(1996).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. IN BRAIN, THE PATTERN OF
CC DISTRIBUTION IS LIMITED TO NEURONS POPULATIONS.
CC -1- DEVELOPMENTAL STAGE: TRANSIENT EXPRESSION BURST IN PURKINJE CELLS
CC AS THE CEREBELLAR CORTEX BECOMES FUNCTIONAL (POSTNATAL DAY 14).
CC AND IN MESENCHYMAL CELLS OF THE DEVELOPING INTERVERTEBRAL DISCS OF
CC THE SPINAL COLUMN.
CC -1- POLYMORPHISM: THE MURINE POLY-GLN REGION IS VERY LIMITED IN
CC COMPARISON TO THE HUMAN SCAL AND IS NOT POLYMORPHIC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X83542; CAA58533.1; -
CC HSP: Q12967; 2RGF.
CC MGD; MGI:104783; Scal.
CC InterPro: IPR003652; Atax_HMG.
CC SMART; SM00536; AXH; 1.
FT DOMAIN 214 217 POLY-PRO.
SQ SEQUENCE 792 AA; 84052 MW; CA5F59C0013499DB CRC64;

Query Match 5.8%; Score 7; DB 1; Length 792;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GLLKALS 65
DB 75 GLLKALS 81
|||||||

RESULT 11
HIG2_HUMAN
ID HIG2_HUMAN STANDARD; PRT; 63 AA.
AC Q9YSL2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOXIA-INDUCIBLE PROTEIN 2.
GN HIG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=20155117; PubMed=10690527;
RA Denko N.C., Schindler C., Koong A., Laderoute K., Green C.,
RA Giaccia A.J.;
RT "Epigenetic regulation of gene expression in cervical cancer cells by
RT the tumor microenvironment.";
RL Clin. Cancer Res. 6:480-487(2000).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
```


CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; AF144755; AAD37585.1; -
CC TRANSMEM 7 23 POTENTIAL.
FT SEQUENCE 63 AA; 6950 MW; 91EA626A511FC8B7 CRC64;
SQ

Query Match 5.0%; Score 6; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SLEGGL 61
DB 26 SLEGGL 31

RESULT 12
SAS2_BACME STANDARD; PRT; 73 AA.
AC F10571;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE SMALL, ACID-SOLUBLE SPORE PROTEIN C2 (SASP).
GN SASP-C2.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85286345; PubMed=3928443;
RA Fliss E.R., Setlow P.;
RT "Genes for Bacillus megaterium small, acid-soluble spore proteins:
RT nucleotide sequence of two genes and their expression during
RT sporulation."
RL Gene 35:151-157(1985).
CC -!- FUNCTION: SASP ARE BOUND TO SPORE DNA. THEY ARE DOUBLE-STRANDED
CC DNA-BINDING PROTEINS THAT CAUSE DNA TO CHANGE TO AN A-LIKE
CC CONFORMATION. THEY PROTECT THE DNA BACKBONE FROM CHEMICAL AND
CC ENZYMIC CLEAVAGE AND ARE THUS INVOLVED IN DORMANT SPORE'S HIGH
CC RESISTANCE TO UV LIGHT.
CC -!- MISCELLANEOUS: SASP ARE DEGRADED IN THE FIRST MINUTES OF SPORE
CC GERMINATION AND PROVIDE AMINO ACIDS FOR BOTH NEW PROTEIN SYNTHESIS
CC AND METABOLISM.
CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-TYPE SASP FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; M10920; -; NOT_ANNOTATED_CDS.
DR PIR; B24033; B24033.
DR InterPro; IPR001448; SASP.
DR Pfam; PF00269; SASP; 1.
DR PROSITE; PS00304; SASP_1; 1.
DR PROSITE; PS00684; SASP_2; 1.
KW DNA-binding; Sporulation; Multigene family.
FT SITE 27 28 CLEAVAGE (BY SPORE PROTEASE).
SQ SEQUENCE 73 AA; 7731 MW; C44EFAFFCAFB24F CRC64;

Query Match 5.0%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GGGRSK 38

DB 65 GGGRSK 70

RESULT 13
SAS5_BACME STANDARD; PRT; 73 AA.
AC P04835;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE SMALL, ACID-SOLUBLE SPORE PROTEIN C5 (SASP).
GN SASP-C5.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86111611; PubMed=3080406;
RA Fliss E.R., Loshon C.A., Setlow P.;
RT "Genes for Bacillus megaterium small, acid-soluble spore proteins:
RT cloning and nucleotide sequence of three additional genes from this
RT multigene family."
RL J. Bacteriol. 165:467-473(1986).
CC -!- FUNCTION: SASP ARE BOUND TO SPORE DNA. THEY ARE DOUBLE-STRANDED
CC DNA-BINDING PROTEINS THAT CAUSE DNA TO CHANGE TO AN A-LIKE
CC CONFORMATION. THEY PROTECT THE DNA BACKBONE FROM CHEMICAL AND
CC ENZYMIC CLEAVAGE AND ARE THUS INVOLVED IN DORMANT SPORE'S HIGH
CC RESISTANCE TO UV LIGHT.
CC -!- MISCELLANEOUS: SASP ARE DEGRADED IN THE FIRST MINUTES OF SPORE
CC GERMINATION AND PROVIDE AMINO ACIDS FOR BOTH NEW PROTEIN SYNTHESIS
CC AND METABOLISM.
CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-TYPE SASP FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; M14111; AAA22284.1;
DR PIR; C24543; C24543.
DR InterPro; IPR001448; SASP.
DR Pfam; PF00269; SASP; 1.
DR PROSITE; PS00304; SASP_1; 1.
DR PROSITE; PS00684; SASP_2; 1.
KW DNA-binding; Sporulation; Multigene family.
FT SITE 27 28 CLEAVAGE (BY SPORE PROTEASE).
SQ SEQUENCE 73 AA; 7680 MW; 5B1455977DC3A025 CRC64;

Query Match 5.0%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GGGRSK 38
DB 65 GGGRSK 70

RESULT 14
Y084_TREPA STANDARD; PRT; 77 AA.
ID Y084_TREPA
AC O83122;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN TP0084.
GN TP0084.
OS Treponema pallidum.

OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT Spirochete";
RL Science 281:375-388(1998).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001193; AAC65088.1; -
DR TIGR; TP0084; -
DR InterPro: IPR000515; BPD_transp.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 77 AA; 8224 MW; 09046A5D92463942 CRC64;

Query Match 5.0%; Score 6; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 ESTSPE 78
Db | | | | |
Db 32 ESTSPE 37

RESULT 15
YJB8_YEAST STANDARD; PRT; 104 AA.
AC P47070;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 11.7 KDA PROTEIN IN PET130-CCT3 INTERGENIC REGION.
GN YJL018W OR J1315.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA To Van D., Perea J., Jacq C.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z49294; CAA89310.1; -
DR SGD; S0003555; YJL018W.
KW Hypothetical protein.
SQ SEQUENCE 104 AA; 11675 MW; A0AA3D1E4C896ACA CRC64;

Query Match 5.0%; Score 6; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 NVPSEFG 112
Db | | | | |
Db 93 NVPSEFG 98

Search completed: May 3, 2002, 12:32:13
Job time: 204 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:28:33 ; Search time 22.27 Seconds
(without alignments)
794.744 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRIMLLFTALAFSLAQSGF.....DVNQENVPFGILKYPPRAE 121

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000.

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	54.5	121	4 Q9UHF0	Q9UHF0 homo sapien
2	10	8.3	116	11 Q9QXS9	Q9QXS9 mus musculus
3	8	6.6	812	2 Q9RT53	Q9RT53 deinoecoccus
4	7	5.8	50	8 Q9BPP5	Q9BPP5 lotus japon
5	7	5.8	98	8 Q9B2G1	Q9B2G1 isodon mac
6	7	5.8	143	2 P73929	P73929 synochocyst
7	7	5.8	286	5 Q9VFR0	Q9VFR0 drosophila
8	7	5.8	297	8 Q03305	Q03305 carettochel
9	7	5.8	348	9 Q9MCB7	Q9MCB7 lactococcus
10	7	5.8	348	9 Q9MCB6	Q9MCB6 lactococcus
11	7	5.8	350	9 Q9MCB8	Q9MCB8 lactococcus
12	7	5.8	366	8 Q9Z255	Q9Z255 neurospora
13	7	5.8	377	2 Q9PH30	Q9PH30 xylella fas
14	7	5.8	388	5 Q44330	Q44330 manduca sex
15	7	5.8	394	2 Q9RVF4	Q9RVF4 deinoecoccus
16	7	5.8	405	5 Q9NFC7	Q9NFC7 drosophila
17	7	5.8	418	2 Q9CLM9	Q9CLM9 pasteurella
18	7	5.8	475	2 Q9PPC5	Q9PPC5 campylobact
19	7	5.8	480	9 Q38300	Q38300 lactococcus

20	7	5.8	481	9 Q38239	Q38239 bacterioph
21	7	5.8	483	10 Q9XE12	Q9XE12 brassica ju
22	7	5.8	493	10 P92947	P92947 arabidopsi
23	7	5.8	493	10 Q9CAK5	Q9CAK5 arabidopsi
24	7	5.8	496	2 Q9HWJ2	Q9HWJ2 pseudomon
25	7	5.8	533	2 Q9Z9N5	Q9Z9N5 bacillus ha
26	7	5.8	534	2 Q9KE54	Q9KE54 bacillus ha
27	7	5.8	608	5 Q9V6D4	Q9V6D4 drosophila
28	7	5.8	637	11 Q9C201	Q9C201 mus musculu
29	7	5.8	702	2 Q9CPW7	Q9CPW7 pasteurella
30	7	5.8	702	10 Q9FR11	Q9FR11 arabidopsi
31	7	5.8	712	5 Q76408	Q76408 caenorhabdi
32	7	5.8	1015	11 Q9D4G5	Q9D4G5 mus musculu
33	7	5.8	1038	10 Q9LE41	Q9LE41 arabidopsi
34	7	5.8	1058	10 Q9LEZ5	Q9LEZ5 arabidopsi
35	7	5.8	1190	10 Q9FNB4	Q9FNB4 arabidopsi
36	7	5.8	1516	10 Q24525	Q24525 arabidopsi
37	7	5.8	3734	3 Q9CLG0	Q9CLG0 kallichroma
38	6	5.0	28	10 Q9S886	Q9S886 citrus sine
39	6	5.0	48	11 Q64224	Q64224 rattus norv
40	6	5.0	49	9 Q9T115	Q9T115 lactobacill
41	6	5.0	63	2 Q9F0S8	Q9F0S8 thermus aqu
42	6	5.0	76	10 Q9M687	Q9M687 gossypium r
43	6	5.0	79	5 Q26801	Q26801 trypanosoma
44	6	5.0	84	12 Q98873	Q98873 turkey herp
45	6	5.0	87	12 Q41132	Q41132 paramecium
46	6	5.0	92	12 Q38024	Q38024 potato viru
47	6	5.0	92	12 Q69331	Q69331 salmairine
48	6	5.0	93	4 Q9UMM4	Q9UMM4 homo sapien
49	6	5.0	93	4 Q9UMM3	Q9UMM3 homo sapien
50	6	5.0	93	4 Q9UMM2	Q9UMM2 homo sapien
51	6	5.0	97	5 Q22828	Q22828 caenorhabdi
52	6	5.0	98	2 P96728	P96728 bacillus su
53	6	5.0	99	10 Q9SBJ6	Q9SBJ6 arabidopsi
54	6	5.0	99	10 Q02024	Q02024 lycopersico
55	6	5.0	99	12 Q9QML0	Q9QML0 human immun
56	6	5.0	100	8 Q9TE67	Q9TE67 felis silve
57	6	5.0	101	12 Q72611	Q72611 human immun
58	6	5.0	101	12 Q97062	Q97062 human immun
59	6	5.0	101	12 Q9QML8	Q9QML8 human immun
60	6	5.0	101	12 Q9Q616	Q9Q616 human immun
61	6	5.0	101	12 Q9Q610	Q9Q610 human immun
62	6	5.0	101	12 Q9DGU6	Q9DGU6 human immun
63	6	5.0	102	12 P88159	P88159 human immun
64	6	5.0	104	11 Q62802	Q62802 rattus norv
65	6	5.0	105	1 O58809	O58809 pyrococcus
66	6	5.0	105	2 Q9KR06	Q9KR06 vibrio chol
67	6	5.0	106	3 P79033	P79033 emericeella
68	6	5.0	108	11 Q9CVC4	Q9CVC4 mus musculu
69	6	5.0	108	12 Q9QNN0	Q9QNN0 potato viru
70	6	5.0	109	5 Q18399	Q18399 caenorhabdi
71	6	5.0	111	4 Q9UI65	Q9UI65 homo sapien
72	6	5.0	111	4 Q9H4W3	Q9H4W3 homo sapien
73	6	5.0	111	11 Q99JK5	Q99JK5 mus musculu
74	6	5.0	117	2 Q9JN12	Q9JN12 agrobacteri
75	6	5.0	120	10 Q02022	Q02022 lycopersico
76	6	5.0	127	5 Q02000	Q02000 chrysaora q
77	6	5.0	128	3 Q93805	Q93805 tricholoma
78	6	5.0	131	11 Q9D2T1	Q9D2T1 mus musculu
79	6	5.0	132	10 Q02021	Q02021 lycopersico
80	6	5.0	133	2 Q9KH64	Q9KH64 uncultured
81	6	5.0	134	2 Q9K3B2	Q9K3B2 uncultured
82	6	5.0	134	2 Q9KJE2	Q9KJE2 lactococcus
83	6	5.0	134	5 P90530	P90530 dictyosteli
84	6	5.0	134	8 Q9G379	Q9G379 felis silve
85	6	5.0	143	9 Q03904	Q03904 bacterioph
86	6	5.0	145	2 Q9RK57	Q9RK57 streptomyc
87	6	5.0	152	1 Q9YANI	Q9YANI aeropyrum p
88	6	5.0	153	1 Q9Y8X9	Q9Y8X9 aeropyrum p
89	6	5.0	156	4 Q14924	Q14924 homo sapien
90	6	5.0	156	11 Q9CQ49	Q9CQ49 mus musculu
91	6	5.0	157	2 Q99YT5	Q99YT5 streptococ
92	6	5.0	160	10 Q39425	Q39425 betula verr

93	6	5.0	160	12	Q9YUD4	Q9YUD4 beak and fe	166	6	5.0	232	2	Q9HYC1	Q9HYC1 pseudomonas
94	6	5.0	161	4	Q9HA90	Q9HA90 homo sapien	167	6	5.0	233	4	Q9BYG2	Q9BYG2 homo sapien
95	6	5.0	162	11	Q9CWF7	Q9CWF7 mus musculus	168	6	5.0	234	1	Q9UWR4	Q9UWR4 uncultured
96	6	5.0	163	2	Q99RA6	Q99RA6 staphylococ	169	6	5.0	238	1	Q9Y9V4	Q9Y9V4 aeropyrum p
97	6	5.0	164	3	P78696	P78696 hirsutella	170	6	5.0	239	3	Q9P3C5	Q9P3C5 neurospora
98	6	5.0	168	5	Q9VWMS	Q9VWMS drosophila	171	6	5.0	239	10	O81430	O81430 arabidopsis
99	6	5.0	169	1	Q27584	Q27584 methanobact	172	6	5.0	239	12	Q9QME3	Q9QME3 avian endog
100	6	5.0	173	5	Q93209	Q93209 caenorhabdi	173	6	5.0	240	2	O9PGT4	O9PGT4 xylella fas
101	6	5.0	173	5	Q9VXB3	Q9VXB3 drosophila	174	6	5.0	240	5	Q9XUP3	Q9XUP3 caenorhabdi
102	6	5.0	174	10	Q9M3T4	Q9M3T4 betulia verr	175	6	5.0	240	13	Q9DEW4	Q9DEW4 raja eglant
103	6	5.0	175	5	Q9G1S5	Q9G1S5 leishmania	176	6	5.0	241	1	Q9HIP9	Q9HIP9 thermoplas
104	6	5.0	177	1	Q29336	Q29336 archaeoglob	177	6	5.0	241	3	Q94436	Q94436 schizosacch
105	6	5.0	179	2	Q44986	Q44986 borrelia af	178	6	5.0	241	12	O11309	O11309 molluscum c
106	6	5.0	179	2	Q44987	Q44987 borrelia af	179	6	5.0	243	10	O9AX45	O9AX45 oryza sativ
107	6	5.0	179	2	Q44988	Q44988 borrelia af	180	6	5.0	243	11	Q9CSK3	Q9CSK3 mus musculu
108	6	5.0	179	8	Q9GAG5	Q9GAG5 polyrbachis	181	6	5.0	246	4	O9S552	O9S552 homo sapien
109	6	5.0	180	2	Q44991	Q44991 borrelia af	182	6	5.0	246	10	O81241	O81241 hellanthus
110	6	5.0	182	2	Q84322	Q84322 chlamydia t	183	6	5.0	246	10	Q9FS15	Q9FS15 arabidopsis
111	6	5.0	182	2	Q84322	Q84322 chlamydia t	184	6	5.0	248	2	Q9KED8	Q9KED8 bacillus ha
112	6	5.0	191	1	Q9YFW9	Q9YFW9 aeropyrum p	185	6	5.0	248	11	Q9CWD5	Q9CWD5 mus musculu
113	6	5.0	191	5	Q9N724	Q9N724 leishmania	186	6	5.0	248	13	O12952	O12952 cynops pyrr
114	6	5.0	191	10	O48763	O48763 arabidopsis	187	6	5.0	250	2	Q9KPF0	Q9KPF0 vibrio chol
115	6	5.0	191	10	O82327	O82327 arabidopsis	188	6	5.0	250	4	O9BR29	O9BR29 synecocyst
116	6	5.0	191	10	Q9C5S0	Q9C5S0 arabidopsis	189	6	5.0	251	2	P73200	P73200 homo sapien
117	6	5.0	193	1	Q9HMG4	Q9HMG4 halobacteri	190	6	5.0	251	5	Q22186	Q22186 caenorhabdi
118	6	5.0	193	2	P94226	P94226 borrelia bu	191	6	5.0	253	5	Q9U8V1	Q9U8V1 branchiosto
119	6	5.0	193	2	O54433	O54433 l plasmodi p	192	6	5.0	258	4	O9H8Q2	O9H8Q2 homo sapien
120	6	5.0	193	2	Q9AC96	Q9AC96 lactococcus	193	6	5.0	261	2	O9BUD2	O9BUD2 homo sapien
121	6	5.0	193	10	O22322	O22322 musa acumin	194	6	5.0	263	2	O9KJ17	O9KJ17 campylobact
122	6	5.0	194	2	Q953P4	Q953P4 borrelia bu	195	6	5.0	263	2	O9X665	O9X665 staphylococ
123	6	5.0	196	10	O48545	O48545 arabidopsis	196	6	5.0	265	2	Q9G925	Q9G925 ochronas
124	6	5.0	197	10	O04369	O04369 lotus japon	197	6	5.0	266	8	Q9G925	Q9G925 staphylococ
125	6	5.0	197	10	O24142	O24142 nicotiana t	198	6	5.0	267	1	O54654	O54654 halobacteri
126	6	5.0	197	10	P92978	P92978 arabidopsis	199	6	5.0	268	4	Q9NS99	Q9NS99 homo sapien
127	6	5.0	197	10	Q9SMC3	Q9SMC3 medicago sa	200	6	5.0	268	10	P81394	P81394 antirrhinum
128	6	5.0	197	10	O9S820	O9S820 nicotiana t	201	6	5.0	270	2	Q9RP27	Q9RP27 haemophilus
129	6	5.0	197	10	O85632	O85632 arabidopsis	202	6	5.0	270	2	Q9R2A8	Q9R2A8 mus musculu
130	6	5.0	198	10	O65062	O65062 picea maria	203	6	5.0	271	11	Q9R2A8	Q9R2A8 mus musculu
131	6	5.0	198	10	Q9ZRD5	Q9ZRD5 arabidopsis	204	6	5.0	273	1	O59396	O59396 pyrococcus
132	6	5.0	199	2	Q9PEA4	Q9PEA4 xylella fas	205	6	5.0	274	1	O9HIQ7	O9HIQ7 thermoplas
133	6	5.0	199	10	O80508	O80508 arabidopsis	206	6	5.0	274	6	Q9GKD9	Q9GKD9 bos taurus
134	6	5.0	202	2	P96506	P96506 borrelia af	207	6	5.0	275	8	Q9S759	Q9S759 kalanchoe f
135	6	5.0	203	2	O50623	O50623 borrelia af	208	6	5.0	275	8	Q9TDT7	Q9TDT7 mesocetoid
136	6	5.0	203	2	P96507	P96507 borrelia af	209	6	5.0	276	2	P72136	P72136 pseudomonas
137	6	5.0	204	12	Q65843	Q65843 beet wester	210	6	5.0	278	5	O17254	O17254 pseudomonas
138	6	5.0	205	4	Q9WTC7	Q9WTC7 homo sapien	211	6	5.0	279	2	Q9KDB7	Q9KDB7 bacillus ha
139	6	5.0	208	10	Q9LQ70	Q9LQ70 arabidopsis	212	6	5.0	280	2	Q9XK11	Q9XK11 streptococ
140	6	5.0	209	2	O54153	O54153 shigella fl	213	6	5.0	283	1	O38143	O38143 archaeoglob
141	6	5.0	209	5	Q9VX73	Q9VX73 drosophila	214	6	5.0	283	11	Q9D412	Q9D412 mus musculu
142	6	5.0	209	10	Q9XG00	Q9XG00 arabidopsis	215	6	5.0	284	10	Q38913	Q38913 arabidopsis
143	6	5.0	211	2	Q49577	Q49577 borrelia af	216	6	5.0	286	2	Q9PPY5	Q9PPY5 ureaplasma
144	6	5.0	212	2	O44669	O44669 borrelia af	217	6	5.0	286	2	Q9PPY5	Q9PPY5 ureaplasma
145	6	5.0	212	2	Q9K1M4	Q9K1M4 borrelia af	218	6	5.0	289	5	Q21150	Q21150 caenorhabdi
146	6	5.0	212	10	Q9FSN7	Q9FSN7 oryza sativ	219	6	5.0	292	2	O9X2C8	O9X2C8 thermotoga
147	6	5.0	212	11	Q99JH8	Q99JH8 mus musculu	220	6	5.0	292	6	Q9GKE0	Q9GKE0 bos taurus
148	6	5.0	216	8	Q9B8Q1	Q9B8Q1 choloeus d	221	6	5.0	293	2	Q9WY20	Q9WY20 thermotoga
149	6	5.0	219	8	Q9TLT3	Q9TLT3 cyanidium c	222	6	5.0	293	5	Q9XTE9	Q9XTE9 caenorhabdi
150	6	5.0	219	8	Q9B9F8	Q9B9F8 prionodon l	223	6	5.0	294	10	Q39533	Q39533 citrullus l
151	6	5.0	219	10	Q9FXC0	Q9FXC0 arabidopsis	224	6	5.0	294	10	O9LGS3	O9LGS3 oryza sativ
152	6	5.0	220	11	Q9QY18	Q9QY18 mus musculu	225	6	5.0	295	5	O62144	O62144 caenorhabdi
153	6	5.0	221	2	Q91302	Q91302 pseudomonas	226	6	5.0	298	5	O61906	O61906 caenorhabdi
154	6	5.0	223	1	O26710	O26710 methanobact	227	6	5.0	299	11	Q9CW34	Q9CW34 mus musculu
155	6	5.0	223	4	Q9H687	Q9H687 homo sapien	228	6	5.0	300	2	Q9L0L3	Q9L0L3 streptomyce
156	6	5.0	224	3	O01680	O01680 pneumocysti	229	6	5.0	302	2	Q9RZU7	Q9RZU7 deinococcus
157	6	5.0	224	4	O9UJF5	O9UJF5 homo sapien	230	6	5.0	305	2	Q9KWC1	Q9KWC1 agrobacteri
158	6	5.0	225	4	Q9BQ99	Q9BQ99 homo sapien	231	6	5.0	305	2	O9F0W2	O9F0W2 pseudomonas
159	6	5.0	225	11	Q9DLJ5	Q9DLJ5 mus musculu	232	6	5.0	306	4	O13962	O13962 homo sapien
160	6	5.0	225	11	Q9CUE2	Q9CUE2 mus musculu	233	6	5.0	309	8	O21043	O21043 dictyosteli
161	6	5.0	227	1	Q9HN05	Q9HN05 halobacteri	234	6	5.0	311	2	Q34127	Q34127 streptococ
162	6	5.0	228	2	Q9L596	Q9L596 heliobacter	235	6	5.0	311	5	Q9V1W8	Q9V1W8 streptococ
163	6	5.0	230	4	O9S553	O9S553 homo sapien	236	6	5.0	312	4	Q9BUV1	Q9BUV1 homo sapien
164	6	5.0	231	1	P95959	P95959 sulfolobus	237	6	5.0	312	10	Q42538	Q42538 arabidopsis
165	6	5.0	231	8	Q02449	Q02449 chlamydomon	238	6	5.0	312	11	Q9DA41	Q9DA41 mus musculu

239	6	5.0	312	11	Q9CWX7	Q9CWX7 mus musculus	312	10	Q9SAW2	Q9SAW2 arabidopsis
240	6	5.0	314	4	Q9H418	Q9H418 homo sapien	313	2	O25835	O25835 helicobacte
241	6	5.0	315	4	Q9POX8	Q9POX8 homo sapien	314	2	Q9ZJY9	Q9ZJY9 helicobacte
242	6	5.0	316	2	Q9C1M8	Q9C1M8 lactococcus	315	2	Q9RYA6	Q9RYA6 deinococcus
243	6	5.0	317	9	Q938317	Q938317 lactobacilli	316	6	Q9C1Z6	Q9C1Z6 pichia past
244	6	5.0	319	2	O66448	O66448 serratia ma	317	6	Q9AZA4	Q9AZA4 lactobacilli
245	6	5.0	319	5	Q9VNJ0	Q9VNJ0 drosophila	318	6	Q14097	Q14097 homo sapien
246	6	5.0	319	10	Q41725	Q41725 zinnia eleg	319	5	O16951	O16951 caenorhabdi
247	6	5.0	319	11	Q9QUH4	Q9QUH4 mus musculus	320	6	Q20405	Q20405 felis silve
248	6	5.0	320	2	O31433	O31433 bacillus su	321	6	O20406	O20406 felis silve
249	6	5.0	320	4	Q9H601	Q9H601 homo sapien	322	6	Q9NFV3	Q9NFV3 lymnaea sta
250	6	5.0	321	4	Q9H601	Q9H601 homo sapien	323	6	Q9NFV2	Q9NFV2 lymnaea sta
251	6	5.0	322	4	Q9H601	Q9H601 homo sapien	324	6	Q9NFV1	Q9NFV1 lymnaea sta
252	6	5.0	322	4	Q9H685	Q9H685 homo sapien	325	6	Q9NFV0	Q9NFV0 lymnaea sta
253	6	5.0	325	11	O61110	O61110 mus musculus	326	6	Q9NFV0	Q9NFV0 lymnaea sta
254	6	5.0	329	5	Q21738	Q21738 caenorhabdi	327	6	Q9NFV1	Q9NFV1 lymnaea sta
255	6	5.0	329	5	Q9CUE7	Q9CUE7 caenorhabdi	328	6	Q9NFV1	Q9NFV1 lymnaea sta
256	6	5.0	329	10	Q43737	Q43737 arabidopsis	329	6	Q9NFV1	Q9NFV1 lymnaea sta
257	6	5.0	329	10	Q9LSY7	Q9LSY7 arabidopsis	330	6	Q9NFV1	Q9NFV1 lymnaea sta
258	6	5.0	330	2	Q9CM09	Q9CM09 pasteurella	331	6	Q9NFV1	Q9NFV1 lymnaea sta
259	6	5.0	331	4	Q9H6D9	Q9H6D9 homo sapien	332	6	Q9NFV1	Q9NFV1 lymnaea sta
260	6	5.0	331	4	Q9H3H6	Q9H3H6 homo sapien	333	6	Q9NFV1	Q9NFV1 lymnaea sta
261	6	5.0	332	3	Q9F887	Q9F887 candida alb	334	6	Q9NFV1	Q9NFV1 lymnaea sta
262	6	5.0	332	10	Q9SCJ7	Q9SCJ7 arabidopsis	335	6	Q9NFV1	Q9NFV1 lymnaea sta
263	6	5.0	333	2	P74586	P74586 synecocyst	336	6	Q9NFV1	Q9NFV1 lymnaea sta
264	6	5.0	333	6	Q9GM09	Q9GM09 macaca fasc	337	6	Q9NFV1	Q9NFV1 lymnaea sta
265	6	5.0	333	10	Q9CAM7	Q9CAM7 arabidopsis	338	6	Q9NFV1	Q9NFV1 lymnaea sta
266	6	5.0	334	2	Q9CHE1	Q9CHE1 lactococcus	339	6	Q9NFV1	Q9NFV1 lymnaea sta
267	6	5.0	334	2	Q9ABN8	Q9ABN8 caulobacter	340	6	Q9NFV1	Q9NFV1 lymnaea sta
268	6	5.0	336	11	Q9R1S6	Q9R1S6 rattus norv	341	6	Q9NFV1	Q9NFV1 lymnaea sta
269	6	5.0	336	13	Q9DD08	Q9DD08 xenopus lae	342	6	Q9NFV1	Q9NFV1 lymnaea sta
270	6	5.0	337	4	Q9P0X7	Q9P0X7 homo sapien	343	6	Q9NFV1	Q9NFV1 lymnaea sta
271	6	5.0	338	11	O88972	O88972 mus musculus	344	6	Q9NFV1	Q9NFV1 lymnaea sta
272	6	5.0	339	12	O40645	O40645 saimirine	345	6	Q9NFV1	Q9NFV1 lymnaea sta
273	6	5.0	340	13	Q9YH20	Q9YH20 gallus gall	346	6	Q9NFV1	Q9NFV1 lymnaea sta
274	6	5.0	341	2	Q9X4N4	Q9X4N4 bacteroides	347	6	Q9NFV1	Q9NFV1 lymnaea sta
275	6	5.0	341	4	Q9P0X6	Q9P0X6 homo sapien	348	6	Q9NFV1	Q9NFV1 lymnaea sta
276	6	5.0	341	6	Q9GMV1	Q9GMV1 canis famil	349	6	Q9NFV1	Q9NFV1 lymnaea sta
277	6	5.0	341	11	Q9QY59	Q9QY59 mus musculus	350	6	Q9NFV1	Q9NFV1 lymnaea sta
278	6	5.0	342	2	Q9A765	Q9A765 caulobacter	351	6	Q9NFV1	Q9NFV1 lymnaea sta
279	6	5.0	342	4	Q9NWK4	Q9NWK4 homo sapien	352	6	Q9NFV1	Q9NFV1 lymnaea sta
280	6	5.0	342	8	Q33761	Q33761 allomyces m	353	6	Q9NFV1	Q9NFV1 lymnaea sta
281	6	5.0	343	2	Q9CHP8	Q9CHP8 lactococcus	354	6	Q9NFV1	Q9NFV1 lymnaea sta
282	6	5.0	344	2	Q9KAP5	Q9KAP5 bacillus ha	355	6	Q9NFV1	Q9NFV1 lymnaea sta
283	6	5.0	344	11	Q9Z246	Q9Z246 mus musculus	356	6	Q9NFV1	Q9NFV1 lymnaea sta
284	6	5.0	345	2	P77585	P77585 escherichia	357	6	Q9NFV1	Q9NFV1 lymnaea sta
285	6	5.0	345	5	Q9WAG3	Q9WAG3 drosophila	358	6	Q9NFV1	Q9NFV1 lymnaea sta
286	6	5.0	345	5	Q9W0R2	Q9W0R2 drosophila	359	6	Q9NFV1	Q9NFV1 lymnaea sta
287	6	5.0	347	2	Q55619	Q55619 synecocyst	360	6	Q9NFV1	Q9NFV1 lymnaea sta
288	6	5.0	347	4	Q9P0Y0	Q9P0Y0 homo sapien	361	6	Q9NFV1	Q9NFV1 lymnaea sta
289	6	5.0	347	10	P93544	P93544 spinacia ol	362	6	Q9NFV1	Q9NFV1 lymnaea sta
290	6	5.0	348	4	Q9BVE3	Q9BVE3 homo sapien	363	6	Q9NFV1	Q9NFV1 lymnaea sta
291	6	5.0	348	5	Q21880	Q21880 caenorhabdi	364	6	Q9NFV1	Q9NFV1 lymnaea sta
292	6	5.0	355	10	O81242	O81242 arabidopsis	365	6	Q9NFV1	Q9NFV1 lymnaea sta
293	6	5.0	355	10	Q9SBE7	Q9SBE7 arabidopsis	366	6	Q9NFV1	Q9NFV1 lymnaea sta
294	6	5.0	357	2	Q9P106	Q9P106 campylobact	367	6	Q9NFV1	Q9NFV1 lymnaea sta
295	6	5.0	359	2	Q9H276	Q9H276 pseudomonas	368	6	Q9NFV1	Q9NFV1 lymnaea sta
296	6	5.0	359	10	Q9SPV4	Q9SPV4 clarkia bre	369	6	Q9NFV1	Q9NFV1 lymnaea sta
297	6	5.0	362	11	O61536	O61536 mus musculus	370	6	Q9NFV1	Q9NFV1 lymnaea sta
298	6	5.0	363	4	Q9P0X9	Q9P0X9 homo sapien	371	6	Q9NFV1	Q9NFV1 lymnaea sta
299	6	5.0	363	5	Q9VGL8	Q9VGL8 drosophila	372	6	Q9NFV1	Q9NFV1 lymnaea sta
300	6	5.0	364	10	O23580	O23580 arabidopsis	373	6	Q9NFV1	Q9NFV1 lymnaea sta
301	6	5.0	365	1	Q9HHX5	Q9HHX5 halobacteri	374	6	Q9NFV1	Q9NFV1 lymnaea sta
302	6	5.0	365	11	Q9D124	Q9D124 mus musculus	375	6	Q9NFV1	Q9NFV1 lymnaea sta
303	6	5.0	366	2	O45378	O45378 bordetella	376	6	Q9NFV1	Q9NFV1 lymnaea sta
304	6	5.0	366	2	O88001	O88001 bordetella	377	6	Q9NFV1	Q9NFV1 lymnaea sta
305	6	5.0	366	2	Q9L1R0	Q9L1R0 streptomyce	378	6	Q9NFV1	Q9NFV1 lymnaea sta
306	6	5.0	368	10	Q9SXN7	Q9SXN7 nicotiana t	379	6	Q9NFV1	Q9NFV1 lymnaea sta
307	6	5.0	370	2	Q9HWH5	Q9HWH5 pseudomonas	380	6	Q9NFV1	Q9NFV1 lymnaea sta
308	6	5.0	371	11	O88178	O88178 rattus norv	381	6	Q9NFV1	Q9NFV1 lymnaea sta
309	6	5.0	372	3	O66813	O66813 saccharomyc	382	6	Q9NFV1	Q9NFV1 lymnaea sta
310	6	5.0	372	5	Q9U116	Q9U116 drosophila	383	6	Q9NFV1	Q9NFV1 lymnaea sta
311	6	5.0	372	5	Q9V117	Q9V117 drosophila	384	6	Q9NFV1	Q9NFV1 lymnaea sta

385	6	5.0	439	2	005912	005912 mycobacteri	458	6	5.0	533	2	Q9R2R6	Q9r2r6 ehrlichia e
386	6	5.0	439	5	096569	096569 drosophila	459	6	5.0	535	8	Q9B6E7	Q9b6e7 yarrowia li
387	6	5.0	439	10	Q9FWD4	Q9fwd4 oryza sativ	460	6	5.0	536	13	Q9PW76	Q9pw76 brachydanio
388	6	5.0	440	2	007334	007334 synechococc	461	6	5.0	541	2	008373	008373 ehrlichia s
389	6	5.0	440	5	Q9GNT1	Q9gnt1 trypanosoma	462	6	5.0	542	5	Q9W0K7	Q9w0k7 drosophila
390	6	5.0	442	2	Q9X2B5	Q9x2b5 thermotoga	463	6	5.0	543	3	Q9C1C8	Q9c1c8 emericella
391	6	5.0	445	2	Q99Q56	Q99q56 staphylococ	464	6	5.0	544	4	Q13652	Q13652 homo sapien
392	6	5.0	446	2	Q9PBX6	Q9pbx6 xylella fas	465	6	5.0	546	5	Q9VMT1	Q9vmt1 drosophila
393	6	5.0	446	2	Q99WE4	Q99we4 staphylococ	466	6	5.0	547	2	Q9XAU7	Q9xau7 alteromonas
394	6	5.0	449	12	Q9PZ18	Q9pz18 xestia c-ni	467	6	5.0	549	2	Q9KG93	Q9kg93 bacillus ha
395	6	5.0	453	10	Q9SEW1	Q9sew1 oryza sativ	468	6	5.0	549	2	Q9AJB5	Q9ajb5 pseudocalter
396	6	5.0	454	4	Q43293	Q43293 homo sapien	469	6	5.0	550	4	Q9HBS2	Q9hbs2 homo sapien
397	6	5.0	454	4	Q9UF99	Q9uf99 homo sapien	470	6	5.0	551	10	Q9LKK00	Q9lkk00 arabidopsis
398	6	5.0	456	5	000834	000834 toxoplasma	471	6	5.0	551	1	Q9HKN7	Q9hkn7 thermoplasm
399	6	5.0	457	2	Q53488	Q53488 micromonosp	472	6	5.0	555	2	Q9X603	Q9x603 primary end
400	6	5.0	457	10	Q9MAI3	Q9mai3 arabidopsis	473	6	5.0	555	13	Q9W791	Q9w791 xenopus lae
401	6	5.0	459	10	Q9XF48	Q9xf48 arabidopsis	474	6	5.0	556	13	Q9W792	Q9w792 brachydanio
402	6	5.0	459	11	Q9JJA1	Q9jja1 mus musculu	475	6	5.0	557	10	Q9SF16	Q9sf16 arabidopsis
403	6	5.0	459	11	Q9CYQ0	Q9cyq0 mus musculu	476	6	5.0	557	12	Q9WR11	Q9wrt1 macaca mula
404	6	5.0	461	2	Q9K498	Q9k498 streptomyce	477	6	5.0	557	12	Q9J2L5	Q9j2l5 macaca mula
405	6	5.0	462	8	Q9BAD4	Q9bad4 brassica na	478	6	5.0	558	5	Q9VJX7	Q9vjx7 drosophila
406	6	5.0	463	13	Q9PW75	Q9pw75 brachydanio	479	6	5.0	560	11	Q9EP84	Q9ep84 mus musculu
407	6	5.0	463	13	Q9PW74	Q9pw74 brachydanio	480	6	5.0	561	12	Q9DK05	Q9dk05 allpahuayo
408	6	5.0	468	2	Q9LAI1	Q9lai1 salmonella	481	6	5.0	561	12	Q9DK04	Q9dk04 allpahuayo
409	6	5.0	469	4	Q14573	Q14573 homo sapien	482	6	5.0	563	5	Q24326	Q24326 drosophila
410	6	5.0	470	2	Q9KAH9	Q9kah9 bacillus ha	483	6	5.0	563	5	Q27933	Q27933 drosophila
411	6	5.0	470	5	Q9VIQ2	Q9viq2 drosophila	484	6	5.0	564	4	Q9UKN4	Q9ukn4 homo sapien
412	6	5.0	472	5	Q20406	Q20406 caenorhabdi	485	6	5.0	564	4	Q9UBW5	Q9ubw5 homo sapien
413	6	5.0	474	5	Q9VQ69	Q9vq69 drosophila	486	6	5.0	565	5	Q21615	Q21615 caenorhabdi
414	6	5.0	475	2	Q9A592	Q9a592 caulobacter	487	6	5.0	568	10	Q9SXD0	Q9sxd0 arabidopsis
415	6	5.0	476	10	P93023	P93023 arabidopsis	488	6	5.0	569	4	Q9BW49	Q9bw49 homo sapien
416	6	5.0	477	10	Q9XID1	Q9xid1 arabidopsis	489	6	5.0	569	11	Q9D0R1	Q9d0r1 mus musculu
417	6	5.0	477	10	Q9FVH4	Q9fvh4 arabidopsis	490	6	5.0	570	4	Q9H6M6	Q9hm6 homo sapien
418	6	5.0	481	3	Q94615	Q94615 schizosacch	491	6	5.0	573	5	Q9GQ09	Q9gqu9 caenorhabdi
419	6	5.0	482	9	Q36165	Q36165 bacterioph	492	6	5.0	576	11	Q70295	Q70295 mus musculu
420	6	5.0	483	10	Q9FL69	Q9fl69 arabidopsis	493	6	5.0	576	11	P97548	P97548 rattus norv
421	6	5.0	484	2	Q56770	Q56770 xanthomonas	494	6	5.0	584	10	Q9SPU1	Q9spu1 oryza sativ
422	6	5.0	485	10	Q65475	Q65475 arabidopsis	495	6	5.0	589	4	Q60541	Q60541 homo sapien
423	6	5.0	487	2	Q9KJX4	Q9kjsx4 myxococcus	496	6	5.0	589	11	Q70296	Q70296 mus musculu
424	6	5.0	491	4	Q9UK46	Q9uk46 homo sapien	497	6	5.0	589	11	P97549	P97549 rattus norv
425	6	5.0	491	6	Q29516	Q29516 cryctolagus	498	6	5.0	590	3	Q24631	Q24631 emericella
426	6	5.0	491	6	Q29532	Q29532 cryctolagus	499	6	5.0	590	3	P93022	P93022 arabidopsis
427	6	5.0	491	11	Q9WUD0	Q9wud0 mus musculu	500	6	5.0	591	10	Q9SG12	Q9sg12 arabidopsis
428	6	5.0	491	11	Q64463	Q64463 mus musculu	501	6	5.0	594	10	Q9FTM9	Q9ftm9 arabidopsis
429	6	5.0	491	11	Q64460	Q64460 mus musculu	502	6	5.0	594	10	Q9CVF3	Q9cvf3 mus musculu
430	6	5.0	491	11	Q64584	Q64584 rattus norv	503	6	5.0	596	11	Q9VTL3	Q9vtl3 drosophila
431	6	5.0	494	11	Q9JJO2	Q9jjo2 rattus norv	504	6	5.0	598	2	Q83032	Q83032 streptomyce
432	6	5.0	496	9	Q9TIC0	Q9tic0 bacterioph	505	6	5.0	599	2	Q9L0I0	Q9l0i0 streptomyce
433	6	5.0	497	5	Q44704	Q44704 caenorhabdi	506	6	5.0	602	2	Q84593	Q84593 chlamydia t
434	6	5.0	499	2	Q9JVT1	Q9jvt1 neisseria m	507	6	5.0	602	2	Q9PJT1	Q9pjf1 chlamydia m
435	6	5.0	502	2	Q9KSU5	Q9ksu5 vibrio chol	508	6	5.0	602	4	Q9H5H5	Q9h5h5 homo sapien
436	6	5.0	502	11	Q9DBF3	Q9dbf3 mus musculu	509	6	5.0	604	13	Q42472	Q42472 xenopus lae
437	6	5.0	503	12	Q39779	Q39779 equine herp	510	6	5.0	605	5	Q45302	Q45302 caenorhabdi
438	6	5.0	504	8	Q9MCX9	Q9mcx9 picummu au	511	6	5.0	605	11	Q62224	Q62224 mus musculu
439	6	5.0	507	2	Q48707	Q48707 lactobacill	512	6	5.0	608	8	Q9B6E6	Q9b6e6 yarrowia li
440	6	5.0	507	5	Q55291	Q55291 caenorhabdi	513	6	5.0	611	2	Q9KLZ8	Q9klz8 vibrio chol
441	6	5.0	507	12	Q9J8C8	Q9j8c8 spodoptera	514	6	5.0	611	5	Q9VTH3	Q9vth3 drosophila
442	6	5.0	508	4	Q9BSS3	Q9bss3 homo sapien	515	6	5.0	621	2	Q9I2T8	Q9i2t8 pseudomonas
443	6	5.0	508	4	Q9PC94	Q9pc94 xylella fas	516	6	5.0	621	4	Q9BTR2	Q9btr2 homo sapien
444	6	5.0	510	5	Q9RY57	Q9ry57 drosophila	517	6	5.0	622	4	Q14859	Q14859 homo sapien
445	6	5.0	511	2	Q9KVQ7	Q9kvq7 deinococcus	518	6	5.0	623	5	Q9VND6	Q9vnd6 drosophila
446	6	5.0	513	3	Q9P6A1	Q9p6a1 neurospora	519	6	5.0	624	11	Q9D2G7	Q9d2g7 mus musculu
447	6	5.0	513	3	Q9XD06	Q9xd06 desulfitoba	520	6	5.0	625	4	Q14677	Q14677 homo sapien
448	6	5.0	515	12	Q56283	Q56283 human herpe	521	6	5.0	628	10	Q9SF51	Q9sf51 arabidopsis
449	6	5.0	516	12	Q9PCG3	Q9pcg3 xylella fas	522	6	5.0	630	4	Q9BR17	Q9br17 homo sapien
450	6	5.0	519	2	Q9LET6	Q9let6 arabidopsis	523	6	5.0	633	10	Q9LZU6	Q9lzu6 arabidopsis
451	6	5.0	527	10	Q9YTP5	Q9ytp5 ateline her	524	6	5.0	635	2	Q9JTR6	Q9jtr6 neisseria m
452	6	5.0	530	2	Q9PNC0	Q9pnc0 campylobact	525	6	5.0	640	4	Q9Y3W8	Q9y3w8 homo sapien
453	6	5.0	530	2	Q9AA00	Q9aa00 caulobacter	526	6	5.0	647	5	Q9V9T1	Q9v9t1 drosophila
454	6	5.0	531	11	Q99KN9	Q99kn9 mus musculu	527	6	5.0	651	2	Q9RDI0	Q9rdi0 streptomyce
455	6	5.0	533	2	Q9S3V5	Q9s3v5 ehrlichia e	528	6	5.0	654	10	Q9ZV25	Q9zv25 arabidopsis
456	6	5.0	533	2	Q9R2R7	Q9r2r7 ehrlichia s	529	6	5.0	656	4	Q9P0U4	Q9p0u4 homo sapien
457	6	5.0	533	2	Q9R2R7	Q9r2r7 ehrlichia s	530	6	5.0				

531	6	5.0	656	4	Q9P2V7	Q9p2v7 homo sapien	604	890	10	Q9LJS0	Q9ljs0 arabidopsis
532	6	5.0	660	11	Q9CWM7	Q9cwm7 mus musculus	605	896	2	Q52618	Q52618 pseudomonas
533	6	5.0	663	8	Q9B6E5	Q9b6e5 yarrowia li	606	896	2	Q52618	Q52618 pseudomonas
534	6	5.0	663	12	Q9B188	Q9b188 molluscum c	607	901	12	P72250	P72250 rhodospirillum rubrum
535	6	5.0	663	12	Q9B188	Q9b188 molluscum c	608	901	12	Q9B188	Q9b188 molluscum c
536	6	5.0	670	4	Q9P1S9	Q9p1s9 homo sapien	609	902	12	Q9B188	Q9b188 molluscum c
537	6	5.0	670	4	Q9P1S9	Q9p1s9 homo sapien	610	905	10	Q9WIT8	Q9wit8 drosophila
538	6	5.0	670	5	Q9P1S9	Q9p1s9 homo sapien	611	907	10	Q9C946	Q9c946 arabidopsis
539	6	5.0	671	10	Q9SKK5	Q9skk5 arabidopsis	612	922	5	Q46354	Q46354 caenorhabditis elegans
540	6	5.0	672	4	Q9NV14	Q9nv14 homo sapien	613	927	3	Q9H3U8	Q9h3u8 homo sapien
541	6	5.0	684	4	Q9UF31	Q9uf31 homo sapien	614	934	10	Q9H3U8	Q9h3u8 homo sapien
542	6	5.0	686	10	Q9STM2	Q9stm2 arabidopsis	615	941	4	Q9H3U8	Q9h3u8 homo sapien
543	6	5.0	689	5	Q9T200	Q9t200 octopus dof	616	941	4	Q9H3U8	Q9h3u8 homo sapien
544	6	5.0	689	5	Q9N2R0	Q9n2r0 loligo peal	617	941	4	Q9H3U8	Q9h3u8 homo sapien
545	6	5.0	690	10	Q9SKK6	Q9skk6 arabidopsis	618	941	4	Q9H3U8	Q9h3u8 homo sapien
546	6	5.0	692	2	Q9O565	Q9o565 bacillus br	619	941	4	Q9H3U8	Q9h3u8 homo sapien
547	6	5.0	695	8	Q9O519	Q9o519 chlorella v	620	941	4	Q9H3U8	Q9h3u8 homo sapien
548	6	5.0	698	10	Q9SDA9	Q9sda9 arabidopsis	621	941	4	Q9H3U8	Q9h3u8 homo sapien
549	6	5.0	701	2	Q9KG92	Q9kg92 bacillus ha	622	942	5	Q18298	Q18298 caenorhabditis elegans
550	6	5.0	702	5	Q9VFR5	Q9vfr5 drosophila	623	942	5	Q18298	Q18298 caenorhabditis elegans
551	6	5.0	706	5	Q9VFR5	Q9vfr5 drosophila	624	944	11	Q99KD5	Q99kd5 mus musculus
552	6	5.0	714	4	Q9HBF9	Q9hbf9 homo sapien	625	949	5	Q94884	Q94884 drosophila
553	6	5.0	720	10	Q9LDM9	Q9ldm9 nicotiana t	626	950	5	Q9VFR5	Q9vfr5 drosophila
554	6	5.0	723	5	Q9V9P5	Q9v9p5 drosophila	627	953	4	Q14151	Q14151 homo sapien
555	6	5.0	727	10	Q9SCF0	Q9scf0 datura stra	628	958	5	Q62397	Q62397 caenorhabditis elegans
556	6	5.0	734	5	Q9K3Z1	Q9k3z1 drosophila	629	962	10	Q9LXK1	Q9lxl1 arabidopsis
557	6	5.0	738	5	Q9K3Z1	Q9k3z1 drosophila	630	963	10	Q93783	Q93783 saccharum o
558	6	5.0	746	6	Q9K3Z1	Q9k3z1 drosophila	631	968	5	Q9VFR5	Q9vfr5 drosophila
559	6	5.0	746	6	Q9K3Z1	Q9k3z1 drosophila	632	973	10	Q9FH17	Q9fhi17 arabidopsis
560	6	5.0	746	6	Q9K3Z1	Q9k3z1 drosophila	633	977	11	Q62269	Q62269 mus musculus
561	6	5.0	746	6	Q9K3Z1	Q9k3z1 drosophila	634	979	5	Q9ULH7	Q9ulh7 drosophila
562	6	5.0	746	6	Q9K3Z1	Q9k3z1 drosophila	635	984	5	Q9XCD4	Q9xcd4 thermomonas
563	6	5.0	746	6	Q9K3Z1	Q9k3z1 drosophila	636	985	5	Q9ULH7	Q9ulh7 drosophila
564	6	5.0	751	2	Q9HVQ1	Q9hvq1 pseudomonas	637	985	5	Q9ULH7	Q9ulh7 drosophila
565	6	5.0	752	2	Q9PEZ5	Q9pfe5 xylella fas	638	991	11	Q62223	Q62223 mus musculus
566	6	5.0	760	10	Q9ZU97	Q9zu97 arabidopsis	639	994	2	Q9ALU6	Q9alu6 pseudomonas
567	6	5.0	761	10	Q9SUH4	Q9suh4 arabidopsis	640	996	5	Q9VFR5	Q9vfr5 drosophila
568	6	5.0	761	10	Q9SUH4	Q9suh4 arabidopsis	641	1004	2	P72226	P72226 pseudomonas
569	6	5.0	770	12	Q98XW9	Q98xw9 emeria bru	642	1007	5	Q17098	Q17098 caenorhabditis elegans
570	6	5.0	772	10	Q9LSB4	Q9lsb4 arabidopsis	643	1008	10	Q9SB51	Q9sb51 arabidopsis
571	6	5.0	780	3	Q9UVE2	Q9uvf2 yarrowia li	644	1011	2	Q9R9F8	Q9rfs8 arabidopsis
572	6	5.0	782	4	Q9BZL4	Q9bz14 homo sapien	645	1014	2	Q55374	Q55374 synechocystis
573	6	5.0	784	5	Q9GTW0	Q9gtw0 caenorhabditis elegans	646	1014	2	Q55374	Q55374 synechocystis
574	6	5.0	793	5	Q9G6B7	Q9g6b7 caenorhabditis elegans	647	1042	5	Q19818	Q19818 caenorhabditis elegans
575	6	5.0	797	4	Q9UQM5	Q9uqm5 homo sapien	648	1047	5	Q22985	Q22985 caenorhabditis elegans
576	6	5.0	800	10	Q9UQM5	Q9uqm5 homo sapien	649	1055	3	Q13397	Q13397 debaryomyces
577	6	5.0	800	11	Q62037	Q62037 mus musculus	650	1061	13	Q9W699	Q9w699 fugu rubrip
578	6	5.0	801	2	Q9EUK6	Q9euh6 salmonella	651	1063	2	Q9CH86	Q9ch86 lactococcus
579	6	5.0	802	2	Q9EUK1	Q9euk1 salmonella	652	1064	5	Q9VFR5	Q9vfr5 drosophila
580	6	5.0	803	2	Q9CIW5	Q9ciw5 lactococcus	653	1068	13	Q42391	Q42391 gallus gall
581	6	5.0	808	13	Q13080	Q13080 xenopus lae	654	1076	3	Q9C1R0	Q9c1r0 debaryomyces
582	6	5.0	808	13	Q9PWK7	Q9pwk7 xenopus lae	655	1082	3	Q13398	Q13398 debaryomyces
583	6	5.0	809	2	Q9R245	Q9rz45 lactococcus	656	1083	12	Q39483	Q39483 avian sarco
584	6	5.0	810	2	Q9CFD3	Q9cfd3 lactococcus	657	1087	5	Q9VFR5	Q9vfr5 drosophila
585	6	5.0	820	2	Q9KUC1	Q9kuc1 vibrio chol	658	1109	8	Q9TL06	Q9tl06 nephroselmis
586	6	5.0	823	2	Q24895	Q24895 helicobacte	659	1125	2	Q9A3K9	Q9a3k9 caulobacter
587	6	5.0	824	2	Q9AAE5	Q9aae5 caulobacter	660	1156	12	P90458	P90458 feline sync
588	6	5.0	831	10	Q64781	Q64781 arabidopsis	661	1160	5	P90935	P90935 caenorhabditis elegans
589	6	5.0	835	5	Q23122	Q23122 caenorhabditis elegans	662	1164	10	Q9SY06	Q9syg6 arabidopsis
590	6	5.0	837	3	Q9HFY8	Q9hfy8 colletotric	663	1165	10	Q9SBK4	Q9sbk4 arabidopsis
591	6	5.0	839	5	Q9BHC2	Q9bhq2 leishmania	664	1165	10	Q9LC25	Q9lc25 arabidopsis
592	6	5.0	840	5	Q9N305	Q9n305 caenorhabditis elegans	665	1166	10	Q9SGV2	Q9sgv2 arabidopsis
593	6	5.0	848	5	Q9V889	Q9v889 drosophila	666	1169	11	Q60502	Q60502 cricetus
594	6	5.0	849	10	Q9SDB0	Q9sdb0 arabidopsis	667	1176	10	Q9FPM4	Q9fpm4 petroselinu
595	6	5.0	853	4	Q9BWH5	Q9bwh5 homo sapien	668	1220	12	Q41894	Q41894 bovine sync
596	6	5.0	856	12	Q41539	Q41539 human immun	669	1225	3	Q9UT00	Q9ut00 schizosacch
597	6	5.0	857	2	Q9KX25	Q9kxx5 streptomyce	670	1226	2	Q9K0W9	Q9kwu9 vibrio chol
598	6	5.0	864	10	Q49329	Q49329 arabidopsis	671	1226	2	Q9AJQ8	Q9ajq8 vibrio fisc
599	6	5.0	881	10	Q9LJS2	Q9ljs2 arabidopsis	672	1234	2	Q912Q2	Q912q2 pseudomonas
600	6	5.0	881	12	Q84735	Q84735 phocine her	673	1236	5	Q9TWA1	Q9twa1 drosophila
601	6	5.0	883	10	Q9LRW9	Q9lrw9 arabidopsis	674	1246	4	Q9V632	Q9v632 homo sapien
602	6	5.0	889	4	Q14917	Q14917 homo sapien	675	1247	5	Q9VNC9	Q9vnc9 drosophila
603	6	5.0	890	10	Q48849	Q48849 arabidopsis	676	1250	2	Q9PPL7	Q9ppl7 campylobact

677	6	5.0	1255	4	Q9BQG0	Q9bqg0 homo sapien	750	6	5.0	3534	12	Q39266	Q39266 equine herp
678	6	5.0	1266	10	Q9LSH3	Q9lsh3 arabidopsis	751	6	5.0	3734	5	Q9BI48	Q9bi48 caenorhabdi
679	6	5.0	1268	10	Q9LUG0	Q9lugo arabidopsis	752	6	5.0	3908	5	Q9BK91	Q9bk91 strongyloce
680	6	5.0	1272	11	Q9TK64	Q9tk64 rattus norv	753	6	5.0	4146	13	Q9BE11	Q9be11 xenopus lae
681	6	5.0	1286	5	P90936	P90936 caenorhabdi	754	6	5.0	7257	2	Q9LC7	Q9lc7 polyanglum
682	6	5.0	1295	3	O13348	O13348 magnaporthe	755	6	5.0	7257	2	Q9LC7	Q9lc7 polyanglum
683	6	5.0	1304	5	Q96959	Q96959 drosophila	756	6	5.0	9376	2	O85168	O85168 pseudomonas
684	6	5.0	1307	5	Q22670	Q22670 caenorhabdi	757	6	5.0	9507	2	Q9EWA1	Q9ewa1 streptomyce
685	6	5.0	1328	4	Q9P0V5	Q9p0v5 homo sapien	758	5	4.1	16	4	Q9UC55	Q9uc55 homo sapien
686	6	5.0	1336	5	Q9VH43	Q9vh43 homo sapien	759	5	4.1	18	2	Q9F581	Q9f581 escherichia
687	6	5.0	1367	5	Q9VYA7	Q9vya7 drosophila	760	5	4.1	20	2	Q46499	Q46499 desulfovibr
688	6	5.0	1371	12	Q9YTP1	Q9ytp1 ateline her	761	5	4.1	21	11	Q9Q0X3	Q9qx3 rattus sp.
689	6	5.0	1377	4	Q9P2A8	Q9p2a8 homo sapien	762	5	4.1	21	12	Q84198	Q84198 paramyxovir
690	6	5.0	1397	10	Q9LP90	Q9lp90 arabidopsis	763	5	4.1	24	7	O77868	O77868 oreochromis
691	6	5.0	1405	10	Q9LHK8	Q9lkh8 arabidopsis	764	5	4.1	24	7	O77869	O77869 oreochromis
692	6	5.0	1413	10	Q9ZUT8	Q9zut8 arabidopsis	765	5	4.1	24	7	O77870	O77870 oreochromis
693	6	5.0	1421	10	O80907	O80907 arabidopsis	766	5	4.1	27	5	Q9BM73	Q9bm73 drosophila
694	6	5.0	1445	10	O80907	O80907 arabidopsis	767	5	4.1	27	12	O56511	O56511 hepatitis c
695	6	5.0	1446	11	Q9QXC1	Q9qxc1 arabidopsis	768	5	4.1	27	12	O56530	O56530 hepatitis c
696	6	5.0	1449	12	O65974	Q65974 mus musculu	769	5	4.1	28	12	Q9QC46	Q9qc46 hepatitis c
697	6	5.0	1450	10	Q9LFH0	Q9lfh0 arabidopsis	770	5	4.1	28	12	Q9QC35	Q9qc35 hepatitis c
698	6	5.0	1456	12	Q9IMP2	Q9imp2 potato viru	771	5	4.1	29	8	Q9G636	Q9g636 calotes lio
699	6	5.0	1504	4	Q9UES6	Q9ues6 homo sapien	772	5	4.1	29	8	Q9G636	Q9g636 calotes lio
700	6	5.0	1510	5	O61802	O61802 caenorhabdi	773	5	4.1	29	8	Q9G600	Q9g600 acanthosaur
701	6	5.0	1519	2	O48237	Q48237 heliocobacte	774	5	4.1	30	4	O14579	O14579 homo sapien
702	6	5.0	1528	4	Q9Y211	Q9y211 homo sapien	775	5	4.1	30	4	Q9UC9	Q9uc9 homo sapien
703	6	5.0	1533	4	O60328	O60328 homo sapien	776	5	4.1	30	5	Q9BM72	Q9bm72 drosophila
704	6	5.0	1547	5	O01940	O01940 drosophila	777	5	4.1	31	10	Q9SMK4	Q9smk4 cicier ariet
705	6	5.0	1547	5	Q9VVF7	Q9vvf7 drosophila	778	5	4.1	33	8	O46929	O46929 joivillea
706	6	5.0	1547	5	Q9VVF7	Q9vvf7 drosophila	779	5	4.1	34	8	O46929	O46929 joivillea
707	6	5.0	1569	5	O00820	O00820 acanthamoeb	780	5	4.1	34	8	O46929	O46929 joivillea
708	6	5.0	1604	13	Q90662	Q90662 gallus gall	781	5	4.1	35	8	O9MFM1	O9mfm1 leopardus p
709	6	5.0	1622	11	Q9Z330	Q9z330 rattus ratt	782	5	4.1	35	8	O9MFM1	O9mfm1 leopardus p
710	6	5.0	1685	4	Q9UEM8	Q9uem8 homo sapien	783	5	4.1	35	8	O9MFM1	O9mfm1 leopardus p
711	6	5.0	1703	13	Q980F7	Q98uf7 fuqu rubrip	784	5	4.1	38	11	Q99N61	Q99n61 rattus norv
712	6	5.0	1711	5	O45409	O45409 caenorhabdi	785	5	4.1	40	10	Q9S927	Q9s927 carpinus be
713	6	5.0	1713	5	Q9V3Q9	Q9v3q9 drosophila	786	5	4.1	41	8	Q9BA11	Q9ba11 hordeum vul
714	6	5.0	1724	5	O96960	O96960 drosophila	787	5	4.1	42	2	O50353	O50353 mycoplasma
715	6	5.0	1738	12	Q39735	Q39735 friend muri	788	5	4.1	42	2	O9R898	O9r898 chlamydia t
716	6	5.0	1752	5	Q9UAK9	Q9uak9 drosophila	789	5	4.1	43	5	O18612	O18612 anemonia su
717	6	5.0	1768	5	Q24153	Q24153 drosophila	790	5	4.1	43	12	Q9Q9X1	Q9q9x1 rift valley
718	6	5.0	1784	10	Q9UC6R1	Q9uc6r1 arabidopsis	791	5	4.1	43	12	Q9Q9X1	Q9q9x1 rift valley
719	6	5.0	1807	4	Q9ULH6	Q9ulh6 homo sapien	792	5	4.1	43	12	Q9Q9W8	Q9q9w8 rift valley
720	6	5.0	1810	5	Q9V483	Q9v483 drosophila	793	5	4.1	43	12	Q9Q9W8	Q9q9w8 rift valley
721	6	5.0	1814	5	Q9V483	Q9v483 drosophila	794	5	4.1	43	12	Q9Q9W8	Q9q9w8 rift valley
722	6	5.0	1872	5	O17083	Q17083 athalia ros	795	5	4.1	43	12	Q9Q9W6	Q9q9w6 rift valley
723	6	5.0	1963	5	O02244	O02244 caenorhabdi	796	5	4.1	43	12	Q9Q9W5	Q9q9w5 rift valley
724	6	5.0	1967	5	Q9VDPV1	Q9vpv1 drosophila	797	5	4.1	43	12	Q9Q9W4	Q9q9w4 rift valley
725	6	5.0	2126	11	Q9UIH7	Q9jih7 rattus norv	798	5	4.1	43	12	Q9Q9W4	Q9q9w4 rift valley
726	6	5.0	2127	12	O57294	O57294 rabies viru	799	5	4.1	43	12	Q9Q9W2	Q9q9w2 rift valley
727	6	5.0	2127	12	Q9JH63	Q9jh63 rabies viru	800	5	4.1	43	12	Q9Q9W2	Q9q9w2 rift valley
728	6	5.0	2127	12	Q9JH63	Q9jh63 rabies viru	801	5	4.1	43	12	Q9Q9W1	Q9q9w1 rift valley
729	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	802	5	4.1	43	12	Q9Q9W0	Q9q9w0 rift valley
730	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	803	5	4.1	43	12	Q9Q9V9	Q9q9v9 rift valley
731	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	804	5	4.1	43	12	Q9Q9V8	Q9q9v8 rift valley
732	6	5.0	2221	5	Q9NKV1	Q9nkv1 halocynthia	805	5	4.1	43	12	Q9Q9V7	Q9q9v7 rift valley
733	6	5.0	2274	11	Q9Z1K7	Q9z1k7 mus musculu	806	5	4.1	43	12	Q9Q9V6	Q9q9v6 rift valley
734	6	5.0	2280	8	Q9MEF2	Q9mef2 oenothera h	807	5	4.1	43	12	Q9Q9V5	Q9q9v5 rift valley
735	6	5.0	2298	8	Q9B1K6	Q9b1k6 lotus japon	808	5	4.1	43	12	Q9Q9V4	Q9q9v4 rift valley
736	6	5.0	2302	5	Q9U9J8	Q9u9j8 caenorhabdi	809	5	4.1	43	12	Q9Q9V3	Q9q9v3 rift valley
737	6	5.0	2303	4	O95996	O95996 homo sapien	810	5	4.1	43	12	Q9Q9V2	Q9q9v2 rift valley
738	6	5.0	2374	5	O45377	O45377 caenorhabdi	811	5	4.1	44	6	Q9TSD3	Q9tsd3 oryctolagus
739	6	5.0	2382	4	Q9H4A3	Q9h4a3 homo sapien	812	5	4.1	44	8	Q9T2T3	Q9t2t3 brassica na
740	6	5.0	2402	2	Q9AER7	Q9aer7 staphylococ	813	5	4.1	44	12	Q69195	Q69195 human cytom
741	6	5.0	2406	5	Q9VXM5	Q9vxm5 drosophila	814	5	4.1	45	2	O9R5Y9	O9r5y9 thermotoga
742	6	5.0	2424	5	Q9VZ48	Q9vz48 drosophila	815	5	4.1	45	2	O9K5Z0	O9k5z0 bacillus h
743	6	5.0	2451	5	Q9VG05	Q9vg05 drosophila	816	5	4.1	45	5	O94692	O94692 polycelis n
744	6	5.0	2489	3	O61116	O61116 saccharomyc	817	5	4.1	46	2	O50700	O50700 borrelia bu
745	6	5.0	2517	3	O9W060	Q9w060 drosophila	818	5	4.1	47	2	O56377	O56377 escherichia
746	6	5.0	2609	3	Q74390	Q74390 schizosacch	819	5	4.1	47	6	Q9GLI7	Q9gli7 sus scrofa
747	6	5.0	2998	5	Q9NKS4	Q9nks4 leishmania	820	5	4.1	48	13	Q9PSR5	Q9psr5 gallus gall
748	6	5.0	3033	12	Q9Q9A7	Q9q9a7 hepatitis c	821	5	4.1	49	2	Q9KM41	Q9km41 vibrio chol
749	6	5.0	3161	2	O54511	O54511 yersinia en	822	5	4.1	50	2	Q9PBF3	Q9pbf3 xytelia fas
			3163	2	Q9Z373	Q9z373 yersinia pe							

823	5	4.1	51	1	Q9HH93	Q9hh93 sulfolobus	896	5	4.1	76	2	Q49255	Q49255 mycoplasma
824	5	4.1	51	2	Q9KIH8	Q9kih8 rhizobium m	897	5	4.1	76	4	Q9UEF4	Q9uef4 homo sapien
825	5	4.1	51	8	Q9MTI3	Q9mti3 oenothera h	898	5	4.1	76	4	Q9H375	Q9h375 homo sapien
826	5	4.1	51	11	Q63905	Q63905 rattus norv	899	5	4.1	76	10	Q9M689	Q9m689 gossypium h
827	5	4.1	52	2	Q9PDF0	Q9pdf0 xyella fas	900	5	4.1	76	10	Q9M686	Q9m686 gossypium h
828	5	4.1	52	12	Q92316	Q92316 human respi	901	5	4.1	76	13	Q9IB49	Q9ib49 pagrus majo
829	5	4.1	52	12	Q92320	Q92320 human respi	902	5	4.1	77	2	Q9B664	Q9b664 streptomyce
830	5	4.1	53	2	Q9PBX9	Q9pbx9 xyella fas	903	5	4.1	77	2	Q9S4W3	Q9s4w3 escherichia
831	5	4.1	53	5	Q9N706	Q9n706 leishmania	904	5	4.1	77	10	Q64565	Q64565 arabidopsis
832	5	4.1	53	14	Q99IS7	Q99is7 uncultured	905	5	4.1	77	10	Q64565	Q64565 arabidopsis
833	5	4.1	54	2	Q9JVE1	Q9jvel neisseria m	906	5	4.1	78	1	Q27316	Q27316 lycopersico
834	5	4.1	54	2	Q9SAS8	Q9sas8 staphylococ	907	5	4.1	78	1	Q9V2Y7	Q9v2y7 methanobact
835	5	4.1	55	4	Q9UGF2	Q9ugf2 homo sapien	908	5	4.1	78	2	P73144	P73144 synchocyst
836	5	4.1	55	8	Q9B795	Q9b795 pytaella l	909	5	4.1	78	2	Q9KCL6	Q9kcl6 bacillus ha
837	5	4.1	55	11	Q93761	Q93761 rattus norv	910	5	4.1	78	3	Q9HGF5	Q9hgf5 saccharomyc
838	5	4.1	56	13	Q9CTK9	Q9ctk9 mus musculu	911	5	4.1	78	11	Q63082	Q63082 rattus norv
839	5	4.1	56	13	Q9PSR7	Q9psr7 gallus gall	912	5	4.1	78	11	Q9JIL5	Q9jil5 rattus norv
840	5	4.1	57	2	Q9K1F2	Q9k1f2 neisseria m	913	5	4.1	79	2	Q9ZL89	Q9ztl89 helicobacte
841	5	4.1	57	2	Q9JUP0	Q9jup0 neisseria m	914	5	4.1	79	2	Q9X3N6	Q9x3n6 brucella me
842	5	4.1	57	10	Q9M3J3	Q9m3j3 spinacia ol	915	5	4.1	79	2	Q9WTF7	Q9wtf7 escherichia
843	5	4.1	57	12	Q69114	Q69114 human herpe	916	5	4.1	79	2	Q9JMR3	Q9jmr3 escherichia
844	5	4.1	57	12	Q69112	Q69112 human herpe	917	5	4.1	79	2	Q9AGY2	Q9agy2 caulobacter
845	5	4.1	58	6	Q9GLG5	Q9glg5 ovis aries	918	5	4.1	79	2	Q9A188	Q9a188 streptococc
846	5	4.1	58	10	Q41336	Q41336 lycopersico	919	5	4.1	79	10	Q64914	Q64914 lycopersico
847	5	4.1	59	2	Q31552	Q31552 bacillus su	920	5	4.1	79	11	Q9Z2U6	Q9z2u6 mus musculu
848	5	4.1	60	8	Q35497	Q35497 paracentrot	921	5	4.1	80	4	Q9BMY8	Q9bmy8 homo sapien
849	5	4.1	61	2	P73064	P73064 synchocyst	922	5	4.1	80	4	Q9G013	Q9g013 bacterioph
850	5	4.1	61	2	Q9K9L2	Q9k9l2 bacillus ha	923	5	4.1	80	9	Q9S963	Q9s963 carpinus be
851	5	4.1	61	11	Q9WVQ2	Q9wvq2 rattus norv	924	5	4.1	80	10	Q9S962	Q9s962 carpinus be
852	5	4.1	62	4	Q15952	Q15952 homo sapien	925	5	4.1	80	10	Q84629	Q84629 paramecium
853	5	4.1	62	4	Q9NRI4	Q9nri4 homo sapien	926	5	4.1	80	12	Q9YVZ7	Q9yvz7 streptomyce
854	5	4.1	62	5	Q96494	Q96494 plasmodium	927	5	4.1	81	2	Q9Z4Y2	Q9z4y2 melanoplus
855	5	4.1	62	5	Q9RZS8	Q9rtzs8 plasmodium	928	5	4.1	81	2	Q9K929	Q9k929 bacillus ha
856	5	4.1	62	13	Q9PSR5	Q9psr5 xenopus . xf	929	5	4.1	81	2	Q9AFW8	Q9afw8 shigella fl
857	5	4.1	63	12	Q72145	Q72145 hantavirus	930	5	4.1	82	1	Q9HPU0	Q9hpu0 halobacteri
858	5	4.1	63	12	Q72146	Q72146 hantavirus	931	5	4.1	82	1	Q9X3N4	Q9x3n4 brucella ab
859	5	4.1	63	12	Q72147	Q72147 hantavirus	932	5	4.1	82	2	Q9SR6	Q9sr6 staphylococ
860	5	4.1	64	2	Q9PEP6	Q9pep6 xyella fas	933	5	4.1	82	2	Q9X3N4	Q9x3n4 caenorhabdi
861	5	4.1	64	11	Q92284	Q92284 rattus norv	934	5	4.1	82	5	Q17981	Q17981 melanochrom
862	5	4.1	64	12	Q90775	Q90775 human herpe	935	5	4.1	82	5	Q9SR6	Q9sr6 staphylococ
863	5	4.1	65	2	Q9RDI8	Q9rdi8 streptomyce	936	5	4.1	82	7	Q31433	Q31433 melanochrom
864	5	4.1	65	10	Q43851	Q43851 triticum ae	937	5	4.1	82	7	Q31440	Q31440 melanochrom
865	5	4.1	65	10	Q9C6P0	Q9c6p0 arabidopsis	938	5	4.1	82	7	Q31450	Q31450 melanochrom
866	5	4.1	66	11	Q61157	Q61157 mus musculu	939	5	4.1	82	7	Q31454	Q31454 melanochrom
867	5	4.1	66	2	P71462	P71462 lactobacilli	940	5	4.1	82	7	Q31455	Q31455 melanochrom
868	5	4.1	66	6	Q9BEF0	Q9bef0 erinaceus e	941	5	4.1	82	7	Q31456	Q31456 melanochrom
869	5	4.1	67	1	P94120	P94120 acidianus a	942	5	4.1	82	7	Q31457	Q31457 melanochrom
870	5	4.1	69	4	Q60786	Q60786 homo sapien	943	5	4.1	82	7	Q31458	Q31458 melanochrom
871	5	4.1	69	4	Q9UDD5	Q9udd5 homo sapien	944	5	4.1	82	7	Q77860	Q77860 oreochromis
872	5	4.1	69	10	Q64913	Q64913 lycopersico	945	5	4.1	82	9	Q80090	Q80090 bacterioph
873	5	4.1	70	4	Q35181	Q35181 homo sapien	946	5	4.1	82	9	Q9MBR1	Q9mbri1 staphylococ
874	5	4.1	71	2	Q9KHU7	Q9khu7 acholeplasm	947	5	4.1	82	9	Q9B0F3	Q9b0f3 staphylococ
875	5	4.1	72	2	Q95230	Q95230 bacillus su	948	5	4.1	82	12	Q91288	Q91288 human immun
876	5	4.1	72	2	Q85497	Q85497 campylobact	949	5	4.1	82	13	Q92094	Q92094 oncorhynch
877	5	4.1	72	2	Q9ALY6	Q9aly6 vibrio para	950	5	4.1	82	13	Q9W7G1	Q9w7g1 oncorhynch
878	5	4.1	72	10	Q9M3P3	Q9m3p3 hordeum sec	951	5	4.1	82	13	Q918Q0	Q918q0 oncorhynch
879	5	4.1	73	2	Q85925	Q85925 sphingomona	952	5	4.1	82	13	Q918P9	Q918p9 oncorhynch
880	5	4.1	73	5	Q21411	Q21411 caenorhabdi	953	5	4.1	83	2	Q9CLW0	Q9clw0 pasteurella
881	5	4.1	73	10	Q9M5K8	Q9m5k8 zea mays (m	954	5	4.1	83	2	Q62096	Q62096 pratylenchu
882	5	4.1	73	12	Q98181	Q98181 molluscum c	955	5	4.1	83	5	Q9U8A5	Q9u8a5 agassizea s
883	5	4.1	74	2	Q50143	Q50143 mycobacteri	956	5	4.1	83	5	Q95042	Q95042 physarum po
884	5	4.1	74	2	Q84450	Q84450 chlamydia t	957	5	4.1	83	7	Q19227	Q19227 rangifer ta
885	5	4.1	74	2	Q9X6M1	Q9x6m1 klebsiella	958	5	4.1	83	10	Q9SFY2	Q9sfy2 arabidopsis
886	5	4.1	74	2	Q9PJU8	Q9pju8 chlamydia m	959	5	4.1	83	10	Q9M445	Q9m445 cicier ariet
887	5	4.1	74	2	Q9LAG8	Q9lag8 streptococc	960	5	4.1	83	12	Q41102	Q41102 paramecium
888	5	4.1	74	2	Q9KCR7	Q9kcr7 bacillus ha	961	5	4.1	84	1	Q9Y8L2	Q9y8l2 aeropyrum p
889	5	4.1	74	4	Q9P193	Q9p193 homo sapien	962	5	4.1	84	2	Q9KND7	Q9knd7 vibrio chol
890	5	4.1	75	2	Q9ZHF4	Q9zhf4 streptococc	963	5	4.1	84	2	Q9A9G1	Q9a9g1 caulobacter
891	5	4.1	75	4	Q9H4S9	Q9h4s9 homo sapien	964	5	4.1	84	3	Q04203	Q04203 saccharomyc
892	5	4.1	75	5	Q96473	Q96473 plasmodium	965	5	4.1	84	5	Q26111	Q26111 pratylenchu
893	5	4.1	75	5	Q9VIA9	Q9via9 drosophila	966	5	4.1	84	10	Q65725	Q65725 brassica na
894	5	4.1	75	10	Q9S860	Q9s860 pisum sativ	967	5	4.1	84	12	Q72917	Q72917 hepatitis c
895	5	4.1	75	10	Q9M688	Q9m688 gossypium h	968	5	4.1	84	12	Q72919	Q72919 hepatitis c

```
969 5 4.1 84 12 072920 072920 hepatitis c
970 5 4.1 84 12 072921 072921 hepatitis c
971 5 4.1 84 12 072922 072922 hepatitis c
972 5 4.1 84 12 072923 072923 hepatitis c
973 5 4.1 84 12 072926 072926 hepatitis c
974 5 4.1 84 12 072927 072927 hepatitis c
975 5 4.1 84 12 072928 072928 hepatitis c
976 5 4.1 84 12 072929 072929 hepatitis c
977 5 4.1 84 12 072930 072930 hepatitis c
978 5 4.1 84 12 072931 072931 hepatitis c
979 5 4.1 85 1 09V2Y9 Q9V2Y9 methanobact
980 5 4.1 85 5 Q26097 Q26097 trypanosoma
981 5 4.1 86 5 Q27360 Q27360 trypanosoma
982 5 4.1 86 12 Q9IHB0 Q9IHB0 human respi
983 5 4.1 87 2 Q9PF42 Q9PF42 xylella fas
984 5 4.1 87 5 Q9VNC7 Q9VNC7 drosophila
985 5 4.1 87 6 Q9PTC4 Q9PTC4 ovis aries
986 5 4.1 87 12 Q9PYU1 Q9PYU1 xestia c-ni
987 5 4.1 87 12 Q9IHB6 Q9IHB6 human respi
988 5 4.1 87 12 Q9IHB3 Q9IHB3 human respi
989 5 4.1 88 2 Q85938 Q85938 sphingomona
990 5 4.1 88 2 Q9Z384 Q9Z384 actinobacil
991 5 4.1 88 2 Q9AIN5 Q9AIN5 candidatus
992 5 4.1 88 2 Q9AIM7 Q9AIM7 candidatus
993 5 4.1 88 2 Q9AIG1 Q9AIG1 candidatus
994 5 4.1 88 5 Q27405 Q27405 pratylenchu
995 5 4.1 88 13 Q9PSY9 Q9PSY9 sparus aura
996 5 4.1 89 2 Q9CF15 Q9CF15 lactococcus
997 5 4.1 89 7 Q9MXW4 Q9MXW4 aotus nancy
998 5 4.1 89 10 Q43665 Q43665 triticum ae
999 5 4.1 90 2 Q54206 Q54206 streptomyce
1000 5 4.1 90 2 Q9FA55 Q9FA55 rhodobacter
```

ALIGNMENTS

```
RESULT 1
Q9UHF0 PRELIMINARY; PRT; 121 AA.
AC Q9UHF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NEUROKININ B-LIKE PROTEIN ZNEUROK1.
GN ZNEUROK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP Sheppard P., Jellinek L., Whitmore T., Blumberg H., Lehner J.,
RA O'Hara P.;
RT "Homo sapiens homolog of neurokinin B.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP Sheppard P., Jellinek L., Whitmore T., Blumberg H., Lehner J.,
RA O'Hara P.;
RT "Homo sapiens homolog of neurokinin B.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE-PLACENTA;
RC MEDLINE-20322570; PubMed-10866201;
RA Page N.M., Woods R.J., Gardner S.M., Lomthasong K., Gladwell R.T.,
RA Butlin D.J., Manyonda I.T., Lowry P.J.;
RT "Excessive placental neurokinin B secretion during the third trimester
RT causes pre-eclampsia.";
RL Nature 405:797-800(2000).
DR EMBL: AF186112; AAF01430.1; -;
DR EMBL: AF216586; AAF76980.1; -;
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_1.
SQ SEQUENCE 121 AA; 13438 MW; 14C9AFE2EB9E9DECA CRC64;
```

Query Match 54.5%; Score 66; DB 4; Length 121;

```
Best Local Similarity 100.0%; Pred. No. 1.le-62;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAOSFGAVCKEPEEVEVGGGRKRDPLYQLQLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAOSFGAVCKEPEEVEVGGGRKRDPLYQLQLFKSHSLEGL 60
QY 61 LKALSQ 66
DB 61 LKALSQ 66
RESULT 2
Q9QXS9 PRELIMINARY; PRT; 116 AA.
AC Q9QXS9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NEUROKININ B-LIKE PROTEIN ZNEUROK1.
GN TAC2 OR ZNEUROK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Sheppard P., Jellinek L., Whitmore T., Blumberg H., Lehner J.,
RA O'Hara P.;
RT "Mus musculus homolog of neurokinin B.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF186116; AAF01434.1; -;
DR MGI: 98476; Tac2.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; UNKNOWN_1.
SQ SEQUENCE 116 AA; 12737 MW; BD4C8B171C2213CC CRC64;
```

```
Query Match 8.3%; Score 10; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFEFG 88
DB 80 KRDMHDFEFG 89
RESULT 3
Q9RT53 PRELIMINARY; PRT; 812 AA.
AC Q9RT53;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DNA GYRASE, SUBUNIT A.
GN DR1913.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R1;
RX MEDLINE-20036996; PubMed-10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Olin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
```

```

DR EMBL; AE002030; AAF11467.1; -.
DR HSPF; P09097; IAB4.
DR TIGR; DR1913; -.
DR InterPro; IPR002205; DNA_topoisomIV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00521; DNA_topoisomIV; 1.
DR SMART; SM00434; TOF4c; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 812 AA; 89824 MW; C6F8596AB57BEC00 CRC64;

Query Match          5.6%; Score 8; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 LEGLLKAL 64
DB 377 LEGLLKAL 384
|||||||

RESULT 4
Q9BBP5 PRELIMINARY; PRT; 50 AA.
AC Q9BBP5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RIBOSOMAL PROTEIN L32.
GN RPL32.
OS Lotus japonicus.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ACCESSION MG-20;
RA Kato T.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ACCESSION MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RT japonicus."
RL DNA Res. 7:323-330(2000).
DR EMBL; AF002983; BAB33243.1; -.
KW Chloroplast.
SQ SEQUENCE 50 AA; 5844 MW; 5589DC533C99ECB6 CRC64;

Query Match          5.8%; Score 7; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AFSLAQS 18
DB 31 AFSLAQS 37
|||||||

RESULT 5
Q9B2G1 PRELIMINARY; PRT; 98 AA.
ID Q9B2G1
AC Q9B2G1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 4L.
GN NADH4L.
OS Isoodon macrourus (Short-nosed bandicoot).

DR EMBL; AE002030; Chordata; Craniata; Vertebrata; Euteleostomi;
DR Mammalia; Metatheria; Peramelemorphia; Peramelidae; Isoodon.
DR NCBI_TaxID=37698;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillips M.J., Lin Y.-H., Harrison G.L., Penny D.;
RT "Mitochondrial Genomes of a Bandicoot and a Brushtail Possum Confirm
RT the Monophyly of Australidelphian Marsupials."
RL Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Lin Y.-H., Phillips M.J.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF358864; AAK38289.1; -.
KW Mitochondrion.
SQ SEQUENCE 98 AA; 10770 MW; 69332F8F406689D4 CRC64;

Query Match          5.8%; Score 7; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ILAFSLA 16
DB 9 ILAFSLA 15
|||||||

RESULT 6
P73929 PRELIMINARY; PRT; 143 AA.
ID P73929
AC P73929;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 15.3 KDA PROTEIN.
GN SLR2101.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
DR EMBL; D90910; BAA17995.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 143 AA; 15349 MW; 67A2C0F7A4BBF15C CRC64;

Query Match          5.8%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 VPSFGIL 114
DB 75 VPSFGIL 81
|||||||

RESULT 7
Q9VFR0 PRELIMINARY; PRT; 286 AA.
ID Q9VFR0
AC Q9VFR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

```

CG9286 PROTEIN.
GN CG9286.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwee R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003701; AAF54990.1; -
DR FlyBase: FBgn0038183; CG9286.
SQ SEQUENCE 286 AA; 32212 MW; 4ADB4B95F2991CD9 CRC64;

Query Match 5.8%; Score 7; DB 5; Length 286;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 QLLQRLF 51
Db 51 QLLQRLF 57

RESULT 8
C003305 PRELIMINARY; PRT; 297 AA.
AC C003305;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Carettochelys insculpta (pitted-shelled turtle).

Mitochondrion.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Trionychioidea; Carettochelyidae;
OC Carettochelys.
OX NCBI_TaxID=44489;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaffer H.B., Meylan P., McKnight M.L.;
RL Syst. Biol. 0:0-0(0).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: OH(2) + 2 FERRICYTOCHROME C -> Q + 2
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: U01355; AAB57646.1; -
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c1; 1.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 297
SQ SEQUENCE 297 AA; 33587 MW; EA3172420509EB1C CRC64;

Query Match 5.8%; Score 7; DB 8; Length 297;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IMLLFTA 9
Db 91 IMLLFTA 97

RESULT 9
Q9MCB7 PRELIMINARY; PRT; 348 AA.
ID Q9MCB7;
AC Q9MCB7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MAJOR CAPSID PROTEIN.
OS Lactococcus lactis bacteriophage Q38.
OC Viruses.
OX NCBI_TaxID=100636;
RN [1]
RP SEQUENCE FROM N.A.
RA Labrie S., Moineau S.;
RT "Multiplex PCR method for the detection and the identification of
RT Lactococcal bacteriophages in cheddar cheese whey."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152411; AAF85637.1; -
SQ SEQUENCE 348 AA; 38887 MW; 9F5C77962A7A4296 CRC64;

Query Match 5.8%; Score 7; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AQSGFVAV 22
Db 273 AQSGFVAV 279

RESULT 10
Q9MCB6

CG9286 PROTEIN.
GN CG9286.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwee R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003701; AAF54990.1; -
DR FlyBase: FBgn0038183; CG9286.
SQ SEQUENCE 286 AA; 32212 MW; 4ADB4B95F2991CD9 CRC64;

Query Match 5.8%; Score 7; DB 5; Length 286;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 QLLQRLF 51
Db 51 QLLQRLF 57

RESULT 8
C003305 PRELIMINARY; PRT; 297 AA.
AC C003305;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Carettochelys insculpta (pitted-shelled turtle).

```

ID Q9MCB6 PRELIMINARY; PRT; 348 AA.
AC Q9MCB6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MAJOR CAPSID PROTEIN.
OS Lactococcus lactis bacteriophage Q44.
OC Viruses.
OX NCBI_TaxID=100638;
RN [1]
RP SEQUENCE FROM N.A.
RA Labrie S., Moineau S.;
RT "Multiplex PCR method for the detection and the identification of
RL Lactococcal bacteriophages in cheddar cheese whey.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152412; AAF85638.1; -
SQ SEQUENCE 348 AA; 38888 MW; 112EC8EC7B512F24 CRC64;

Query Match 5.8%; Score 7; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AQSFGAV 22
Db 273 AQSFGAV 279
|||||

RESULT 11
Q9MCB8 PRELIMINARY; PRT; 350 AA.
ID Q9MCB8;
AC Q9MCB8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MAJOR CAPSID PROTEIN.
OS Lactococcus lactis bacteriophage ebl.
OC Viruses.
OX NCBI_TaxID=100640;
RN [1]
RP SEQUENCE FROM N.A.
RA Labrie S., Moineau S.;
RT "Multiplex PCR method for the detection and the identification of
RL Lactococcal bacteriophages in cheddar cheese whey.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152410; AAF85636.1; -
SQ SEQUENCE 350 AA; 38954 MW; 552FD83845DF2960 CRC64;

Query Match 5.8%; Score 7; DB 9; Length 350;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AQSFGAV 22
Db 273 AQSFGAV 279
|||||

RESULT 12
Q9ZZ55 PRELIMINARY; PRT; 366 AA.
ID Q9ZZ55;
AC Q9ZZ55;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MATURASE.
OS Neurospora crassa.
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RX MEDLINE-85033713; PubMed-6238172;
RA Morelli G., Macino G.;
RT "Two intervening sequences in the ATPase subunit 6 gene of Neurospora
RT crassa. A short intron (93 base-pairs) and a long intron that is
RT stable after excision.";
RL J. Mol. Biol. 178:491-507(1984).
DR EMBL; X01075; CAA25541.1; -
DR InterPro; IPR001982; Intron_endonuc.
DR Pfam; PF00961; Intron_maturase; 2.
KW Mitochondrion.
SQ SEQUENCE 366 AA; 42285 MW; 8AAA7BAA442BA9FA CRC64;

Query Match 5.8%; Score 7; DB 8; Length 366;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SLEGLLK 62
Db 178 SLEGLLK 184
|||||

RESULT 13
Q9PH30 PRELIMINARY; PRT; 377 AA.
ID Q9PH30;
AC Q9PH30;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE.
GN XF0116.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003865; AAF82929.1; -
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF01546; Peptidase_M20; 1.
KW Complete proteome.
SQ SEQUENCE 377 AA; 40723 MW; 1FB7EDM4ACA2E5B8 CRC64;
```

Query Match 5.8%; Score 7; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 PDLXQLL 47
 Db 363 PDLXQLL 369
 |||||

RESULT 14
 O44330 PRELIMINARY; PRT; 388 AA.
 AC O44330;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE HEMOCYTE PROTEASE-1.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Sphingioidea; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Wang Y., Kanost M.R.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
 CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
 DR EMBL; AF017663; AAB94557.1;
 DR HSP; P00750; IRTF.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 388 AA; 43500 MW; C6134391EF2AE47C CRC64;

Query Match 5.8%; Score 7; DB 5; Length 388;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GGRSKR 39
 Db 39 GGRSKR 45
 |||||

RESULT 15
 Q9RVF4 PRELIMINARY; PRT; 394 AA.
 AC Q9RVF4;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE DE CONSERVED HYPOTHETICAL PROTEIN.
 GN DR1075.
 OS Deinococcus radiodurans.
 CC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-R1.
 RX MEDLINE-20036896; PubMed-10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,

RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL; AE001958; AAF10648.1; -.
 DR TIGR; DR1075; -.
 KW Complete proteome.
 SQ SEQUENCE 394 AA; 42220 MW; D4EE13E37BA5EABE CRC64;

Query Match 5.8%; Score 7; DB 2; Length 394;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLFTAIL 11
 Db 34 LLFTAIL 40
 |||||

Search completed: May 3, 2002, 12:32:02
 Job time: 209 sec

